

# Sequence Listing

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 Gerber, Hanspeter  
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 Goddard, Audrey  
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 Hillan, Kenneth J  
 Kljavin, Ivar J.  
 Kuo, Sophia S.  
 Napier, Mary A.  
 Pan, James;  
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Ser	Leu	Tyr	Met	Gly	Ala	Leu	Val	Arg	Cys	Thr	Thr	Leu	Cys	Leu					
				200					205					210					
Gly	Tyr	Tyr	Lys	Asn	Ile	His	Asp	Ile	Ile	Pro	Asp	Arg	Ser	Gly					
				215					220					225					
Pro	Glu	Leu	Gly	Gly	Asp	Ala	Thr	Ile	Arg	Lys	Met	Leu	Ser	Phe					
				230					235					240					
Trp	Trp	Pro	Leu	Ala	Leu	Ile	Leu	Ala	Thr	Gln	Arg	Ile	Ser	Arg					
				245					250					255					
Pro	Ile	Val	Asn	Leu	Phe	Val	Ser	Arg	Asp	Leu	Gly	Gly	Ser	Ser					
				260					265					270					
Ala	Ala	Thr	Glu	Ala	Val	Ala	Ile	Leu	Thr	Ala	Thr	Tyr	Pro	Val					
				275					280					285					
Gly	His	Met	Pro	Tyr	Gly	Trp	Leu	Thr	Glu	Ile	Arg	Ala	Val	Tyr					
				290					295					300					
Pro	Ala	Phe	Asp	Lys	Asn	Asn	Pro	Ser	Asn	Lys	Leu	Val	Ser	Thr					
				305					310					315					
Ser	Asn	Thr	Val	Thr	Ala	Ala	His	Ile	Lys	Lys	Phe	Thr	Phe	Val					
				320					325					330					
Cys	Met	Ala	Leu	Ser	Leu	Thr	Leu	Cys	Phe	Val	Met	Phe	Trp	Thr					
				335					340					345					

Pro	Asn	Val	Ser	Glu	Lys	Ile	Leu	Ile	Asp	Ile	Ile	Gly	Val	Asp
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Phe	Ala	Phe	Ala	Glu	Leu	Cys	Val	Val	Pro	Leu	Arg	Ile	Phe	Ser
				365					370					375
Phe	Phe	Pro	Val	Pro	Val	Thr	Val	Arg	Ala	His	Leu	Thr	Gly	Trp
				380					385					390
Leu	Met	Thr	Leu	Lys	Lys	Thr	Phe	Val	Leu	Ala	Pro	Ser	Ser	Val
				395					400					405
Leu	Arg	Ile	Ile	Val	Leu	Ile	Ala	Ser	Leu	Val	Val	Leu	Pro	Tyr
				410					415					420
Leu	Gly	Val	His	Gly	Ala	Thr	Leu	Gly	Val	Gly	Ser	Leu	Leu	Ala
				425					430					435
Gly	Phe	Val	Gly	Glu	Ser	Thr	Met	Val	Ala	Ile	Ala	Ala	Cys	Tyr
				440					445					450
Val	Tyr	Arg	Lys	Gln	Lys	Lys	Lys	Met	Glu	Asn	Glu	Ser	Ala	Thr
				455					460					465
Glu	Gly	Glu	Asp	Ser	Ala	Met	Thr	Asp	Met	Pro	Pro	Thr	Glu	Glu
				470					475					480
Val	Thr	Asp	Ile	Val	Glu	Met	Arg	Glu	Glu	Asn	Glu			
				485					490					

<210> 8  
 <211> 535  
 <212> DNA  
 <213> Homo sapiens

<220>  
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 <222> 33, 66, 96, 387  
 <223> unknown base

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 cggcctattg tcaacctctt tgtttcccg gaccttggtg gcagttctgc 150  
 agccacagag gcagtggcga ttttgacagc cacataccct gtgggtcaca 200  
 tgccatacgg ctggttgacg gaaatccgtg ctgtgtatcc tgctttcgac 250  
 aagaataacc ccagcaacaa actggtgagc acgagcaaca cagtcacggc 300  
 ggccacatc aagaagttca ccttcgtctg catggctctg tctctcacgc 350  
 tctgtttcgt gatgttttgg acaccaacg tgtctgngaa aatcttgata 400  
 gacatcatcg gagtggactt tgcctttgca gaactctgtg ttgttccttt 450

gcgggatcttc tccttcttcc cagttccagt cacagtgagg gcgcatctca 500  
ccgggtgggt gatgacactg aagaaaacct tcgtc 535

<210> 9  
<211> 434  
<212> DNA  
<213> Homo sapiens

<220>  
<221> unsure  
<222> 32, 54, 80, 111, 117, 122, 139, 193, 205, 221, 226, 293, 296, 305, 336, 358, 361  
<223> unknown base

<400> 9  
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caanaaattg gggagcaggg caaacagtn acgggcagcc cacatcaaga 100  
agttcacctt ngtttgnatg gntctgtcaa ctcacgctnt gtttcgtgat 150  
gttttgagaca ccaaagtgt ttgagaaaat tttgatagac atnatcggag 200  
tggantttgc ctttgcagaa ntttgngntg ttcctttgcg gattttctcc 250  
ttttcccag ttccagtcac agngagggcg catctcaccg gnggntgat 300  
gacantgaag aaaacctttg tccttgcccc cagctntttg gtgcggatca 350  
ttgtcctnat ngccagcctt gtggtcctac cctacctggg ggtgcacggt 400  
gcgaccttg gcgtgggttc cctcctggcg ggca 434

<210> 10  
<211> 154  
<212> DNA  
<213> Homo sapiens

<220>  
<221> unsure  
<222> 33, 49, 68, 83, 90, 98, 119  
<223> unknown base

<400> 10  
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aactgaaga aaaccttngt ccttgcccc agntttgtgn tgcggatnat 100  
cgtcctcatc gccagcctng tggctctacc ctacctgggg gtgcacggtg 150  
agac 154

<210> 11  
<211> 24  
<212> DNA  
<213> Artificial Sequence



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<220>
<223> Synthetic oligonucleotide probe

<400> 11
ctgatccggt tcttggtgcc cctg 24

<210> 12
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 12
gctctgtcac tcacgctc 18

<210> 13
<211> 18
<212> DNA
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<220>
<223> Synthetic oligonucleotide probe

<400> 13
tcattctcttc cctctccc 18

<210> 14
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 14
ccttccgcca cggagttc 18

<210> 15
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 15
ggcaaagtcc actccgatga tgct 24

<210> 16
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

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Leu	Leu	Gly	Tyr	Arg	Ala	Val	Tyr	Arg	Met	Cys	Phe	Ala	Thr	Ala		95	100	105
Ala	Phe	Phe	Phe	Phe	Phe	Phe	Thr	Leu	Leu	Met	Leu	Cys	Val	Ser		110	115	120
Ser	Ser	Arg	Asp	Pro	Arg	Ala	Ala	Ile	Gln	Asn	Gly	Phe	Trp	Phe		125	130	135
Phe	Lys	Phe	Leu	Ile	Leu	Val	Gly	Leu	Thr	Val	Gly	Ala	Phe	Tyr		140	145	150
Ile	Pro	Asp	Gly	Ser	Phe	Thr	Asn	Ile	Trp	Phe	Tyr	Phe	Gly	Val		155	160	165
Val	Gly	Ser	Phe	Leu	Phe	Ile	Leu	Ile	Gln	Leu	Val	Leu	Leu	Ile		170	175	180
Asp	Phe	Ala	His	Ser	Trp	Asn	Gln	Arg	Trp	Leu	Gly	Lys	Ala	Glu		185	190	195
Glu	Cys	Asp	Ser	Arg	Ala	Trp	Tyr	Ala	Gly	Leu	Phe	Phe	Phe	Thr		200	205	210
Leu	Leu	Phe	Tyr	Leu	Leu	Ser	Ile	Ala	Ala	Val	Ala	Leu	Met	Phe		215	220	225
Met	Tyr	Tyr	Thr	Glu	Pro	Ser	Gly	Cys	His	Glu	Gly	Lys	Val	Phe		230	235	240
Ile	Ser	Leu	Asn	Leu	Thr	Phe	Cys	Val	Cys	Val	Ser	Ile	Ala	Ala		245	250	255
Val	Leu	Pro	Lys	Val	Gln	Asp	Ala	Gln	Pro	Asn	Ser	Gly	Leu	Leu		260	265	270
Gln	Ala	Ser	Val	Ile	Thr	Leu	Tyr	Thr	Met	Phe	Val	Thr	Trp	Ser		275	280	285
Ala	Leu	Ser	Ser	Ile	Pro	Glu	Gln	Lys	Cys	Asn	Pro	His	Leu	Pro		290	295	300
Thr	Gln	Leu	Gly	Asn	Glu	Thr	Val	Val	Ala	Gly	Pro	Glu	Gly	Tyr		305	310	315
Glu	Thr	Gln	Trp	Trp	Asp	Ala	Pro	Ser	Ile	Val	Gly	Leu	Ile	Ile		320	325	330
Phe	Leu	Leu	Cys	Thr	Leu	Phe	Ile	Ser	Leu	Arg	Ser	Ser	Asp	His		335	340	345
Arg	Gln	Val	Asn	Ser	Leu	Met	Gln	Thr	Glu	Glu	Cys	Pro	Pro	Met				

	350		355		360
Leu Asp Ala Thr	Gln Gln Gln Gln Gln	Gln Val Ala Ala Cys	Glu		
	365		370		375
Gly Arg Ala Phe	Asp Asn Glu Gln Asp	Gly Val Thr Tyr Ser	Tyr		
	380		385		390
Ser Phe Phe His	Phe Cys Leu Val Leu	Ala Ser Leu His Val	Met		
	395		400		405
Met Thr Leu Thr	Asn Trp Tyr Lys Pro	Gly Glu Thr Arg Lys	Met		
	410		415		420
Ile Ser Thr Trp	Thr Ala Val Trp Val	Lys Ile Cys Ala Ser	Trp		
	425		430		435
Ala Gly Leu Leu	Leu Tyr Leu Trp Thr	Leu Val Ala Pro Leu	Leu		
	440		445		450
Leu Arg Asn Arg	Asp Phe Ser				
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<220>  
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<210> 21  
 <211> 20  
 <212> DNA  
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<220>  
 <223> Synthetic oligonucleotide probe

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<210> 22  
 <211> 20  
 <212> DNA  
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<220>  
 <223> Synthetic oligonucleotide probe

<400> 22  
 cttcttccac ttctgcctgg 20

<210> 23  
 <211> 18

<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 23  
cctgggcaaa aatgcaac 18

<210> 24  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 24  
caggaatgta gaaggcaccc acgg 24

<210> 25  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 25  
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<210> 26  
<211> 50  
<212> DNA  
<213> Artificial Sequence

<220>  
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<210> 27  
<211> 1351  
<212> DNA  
<213> Homo sapiens

<400> 27  
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cgcggcacgt ccgcgaggac ttgaagtcct gagcgctcaa gtttgtccgt 150  
aggtcgagag aaggccatgg aggtgccgcc accggcaccg cggagctttc 200  
tctgtagagc attgtgccta tttccccgag tctttgctgc cgaagctgtg 250

actgcogatt cggaagtcct tgaggagcgt cagaagcggc ttccctacgt 300  
 cccagagccc tattaccggg aatctggatg ggaccgcctc cgggagctgt 350  
 ttggcaaaga tgaacagcag agaatttcaa aggaccttgc taatatctgt 400  
 aagacggcag ctacagcagg catcattggc tgggtgtatg ggggaatacc 450  
 agctttttatt catgctaaac aacaatacat tgagcagagc caggcagaaa 500  
 tttatcataa cgggtttgat gctgtgcaat ctgcacatcg tgctgccaca 550  
 cgaggcttca ttogttatgg ctggcgctgg ggttggagaa ctgcagtgtt 600  
 tgtgactata ttcaacacag tgaacactag tctgaatgta taccgaaata 650  
 aagatgcctt aagccatttt gtaattgcag gagctgtcac gggaagtctt 700  
 tttaggataa acgtaggcct gcgtggcctg gtggctggtg gcataattgg 750  
 agccttgctg ggcaactcct taggaggcct gctgatggca tttcagaagt 800  
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 ttaatctatc aatatatgca tacatggata tatccacca cctagatttt 1300  
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<210> 28

<211> 285

<212> PRT

<213> Homo sapiens

<400> 28

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Leu	Cys	Leu	Phe	Pro	Arg	Val	Phe	Ala	Ala	Glu	Ala	Val	Thr	Ala
				20				25					30	

Asp	Ser	Glu	Val	Leu	Glu	Glu	Arg	Gln	Lys	Arg	Leu	Pro	Tyr	Val	35	40	45
Pro	Glu	Pro	Tyr	Tyr	Pro	Glu	Ser	Gly	Trp	Asp	Arg	Leu	Arg	Glu	50	55	60
Leu	Phe	Gly	Lys	Asp	Glu	Gln	Gln	Arg	Ile	Ser	Lys	Asp	Leu	Ala	65	70	75
Asn	Ile	Cys	Lys	Thr	Ala	Ala	Thr	Ala	Gly	Ile	Ile	Gly	Trp	Val	80	85	90
Tyr	Gly	Gly	Ile	Pro	Ala	Phe	Ile	His	Ala	Lys	Gln	Gln	Tyr	Ile	95	100	105
Glu	Gln	Ser	Gln	Ala	Glu	Ile	Tyr	His	Asn	Arg	Phe	Asp	Ala	Val	110	115	120
Gln	Ser	Ala	His	Arg	Ala	Ala	Thr	Arg	Gly	Phe	Ile	Arg	Tyr	Gly	125	130	135
Trp	Arg	Trp	Gly	Trp	Arg	Thr	Ala	Val	Phe	Val	Thr	Ile	Phe	Asn	140	145	150
Thr	Val	Asn	Thr	Ser	Leu	Asn	Val	Tyr	Arg	Asn	Lys	Asp	Ala	Leu	155	160	165
Ser	His	Phe	Val	Ile	Ala	Gly	Ala	Val	Thr	Gly	Ser	Leu	Phe	Arg	170	175	180
Ile	Asn	Val	Gly	Leu	Arg	Gly	Leu	Val	Ala	Gly	Gly	Ile	Ile	Gly	185	190	195
Ala	Leu	Leu	Gly	Thr	Pro	Val	Gly	Gly	Leu	Leu	Met	Ala	Phe	Gln	200	205	210
Lys	Tyr	Ala	Gly	Glu	Thr	Val	Gln	Glu	Arg	Lys	Gln	Lys	Asp	Arg	215	220	225
Lys	Ala	Leu	His	Glu	Leu	Lys	Leu	Glu	Glu	Trp	Lys	Gly	Arg	Leu	230	235	240
Gln	Val	Thr	Glu	His	Leu	Pro	Glu	Lys	Ile	Glu	Ser	Ser	Leu	Arg	245	250	255
Glu	Asp	Glu	Pro	Glu	Asn	Asp	Ala	Lys	Lys	Ile	Glu	Ala	Leu	Leu	260	265	270
Asn	Leu	Pro	Arg	Asn	Pro	Ser	Val	Ile	Asp	Lys	Gln	Asp	Lys	Asp	275	280	285

<210> 29

<211> 324

<212> DNA

<213> Homo sapiens

<400> 29

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<400> 32  
cttgaggagc gtcagaagcg 20

<210> 33  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 33  
ataacgaatg aagcctcgtg 20

<210> 34  
<211> 40  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 34  
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<210> 35  
<211> 1819  
<212> DNA  
<213> Homo sapiens

<400> 35  
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tccgagtggc cggcgtggc attgcagtgg gcatcttctt gttcctgatt 350  
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 atctcccata atttgaaatt gaaatcgtat tgtgtggctc tgtatattct 1750  
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<210> 36

<211> 204

<212> PRT

<213> Homo sapiens

<400> 36

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Leu	Asn	Leu	Leu	Tyr	Thr	Leu	Val	Ser	Leu	Leu	Leu	Ile	Gly	Ile
				20					25					30

Ala	Ala	Trp	Gly	Ile	Gly	Phe	Gly	Leu	Ile	Ser	Ser	Leu	Arg	Val	
				35					40					45	
Val	Gly	Val	Val	Ile	Ala	Val	Gly	Ile	Phe	Leu	Phe	Leu	Ile	Ala	
				50					55					60	
Leu	Val	Gly	Leu	Ile	Gly	Ala	Val	Lys	His	His	Gln	Val	Leu	Leu	
				65					70					75	
Phe	Phe	Tyr	Met	Ile	Ile	Leu	Leu	Leu	Val	Phe	Ile	Val	Gln	Phe	
				80					85					90	
Ser	Val	Ser	Cys	Ala	Cys	Leu	Ala	Leu	Asn	Gln	Glu	Gln	Gln	Gly	
				95					100					105	
Gln	Leu	Leu	Glu	Val	Gly	Trp	Asn	Asn	Thr	Ala	Ser	Ala	Arg	Asn	
				110					115					120	
Asp	Ile	Gln	Arg	Asn	Leu	Asn	Cys	Cys	Gly	Phe	Arg	Ser	Val	Asn	
				125					130					135	
Pro	Asn	Asp	Thr	Cys	Leu	Ala	Ser	Cys	Val	Lys	Ser	Asp	His	Ser	
				140					145					150	
Cys	Ser	Pro	Cys	Ala	Pro	Ile	Ile	Gly	Glu	Tyr	Ala	Gly	Glu	Val	
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Leu	Arg	Phe	Val	Gly	Gly	Ile	Gly	Leu	Phe	Phe	Ser	Phe	Thr	Glu	
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Ile	Leu	Gly	Val	Trp	Leu	Thr	Tyr	Arg	Tyr	Arg	Asn	Gln	Lys	Asp	
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Pro	Arg	Ala	Asn	Pro	Ser	Ala	Phe	Leu							
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<210> 37  
 <211> 390  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> unsure  
 <222> 20, 35, 61, 83, 106, 130, 133, 187, 232, 260, 336  
 <223> unknown base

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 tagccntgaa ccaggagcaa cagggtcagn ttntggaggt tggttggaac 150  
 aatacggcaa gtgctcgaaa tgacatccag agaaatntaa actgctgtgg 200  
 gttccgaagt gttaacccaa atgacacctg tntggctagc tgtgttaaaa 250  
 gtgaccactn gtgctcgcca tgtgtcccaa tcataggaga atatgctgga 300

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<210> 38  
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<212> DNA  
<213> Homo sapiens

<220>  
<221> unsure  
<222> 27  
<223> unknown base

<400> 38  
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tttttgactt ttacaggtaa gtgcaaagga gaagtgggtt catgaaatgt 200  
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taatttgaag tctaaaagac tgcattttta aacaagttag tattaatgcg 350  
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ccgttttcat gaaagtctc agtattgtaa cagcaacttg tcaaacctaa 450  
gcatatttga atatgatctc ccataatttg aaattgaaat cgtatttgtgt 500  
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gttgtgcccc acttgc 566

<210> 39  
<211> 264  
<212> DNA  
<213> Homo sapiens

<220>  
<221> unsure  
<222> 84-85, 206  
<223> unknown base

<400> 39  
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tggttggtgcaa caatcacggc caagtgactc cgcaaatgac atcccagaga 150  
aatcctaaac tgctgtgggt tccgaagtgt taaccocaaat gacacctgtc 200

tggctngctg tggtaaaagt gaccactcgt gctcgccatg tgctccaatc 250  
 ataggagaat atgc 264  
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 <223> Synthetic oligonucleotide probe  
 <400> 41  
 gagaatatgc tggagagg 18  
 <210> 42  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence  
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 <223> Synthetic oligonucleotide probe  
 <400> 42  
 aggaatgcac taggattcgc gcgg 24  
 <210> 43  
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 <212> DNA  
 <213> Artificial Sequence  
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 <400> 43  
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 <210> 44  
 <211> 2061  
 <212> DNA  
 <213> Homo sapiens  
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gagcgtgcag tgtgagggac ctgtctgcac tgaggagagc agctgccaca 150  
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agctaactca cccttccacc atatgaggac gtggcaagaa gatgacatgt 1950  
atgagaacca aaaaacagct gtcgccaaac accgactctg tcgttgccct 2000  
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ttgtagccta a 2061

<210> 45

<211> 359

<212> PRT

<213> Homo sapiens

<400> 45

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Leu	Gly	Val	Leu	Trp	Val	Ala	Gln	Met	Leu	Leu	Ala	Ala	Ser	Phe
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Glu	Thr	Leu	Gln	Cys	Glu	Gly	Pro	Val	Cys	Thr	Glu	Glu	Ser	Ser
				35					40					45
Cys	His	Thr	Glu	Asp	Asp	Leu	Thr	Asp	Ala	Arg	Glu	Ala	Gly	Phe
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Gln	Val	Lys	Ala	Tyr	Thr	Phe	Ser	Glu	Pro	Phe	His	Leu	Ile	Val
				65					70					75
Ser	Tyr	Asp	Trp	Leu	Ile	Leu	Gln	Gly	Pro	Ala	Lys	Pro	Val	Phe
				80					85					90
Glu	Gly	Asp	Leu	Leu	Val	Leu	Arg	Cys	Gln	Ala	Trp	Gln	Asp	Trp
				95					100					105
Pro	Leu	Thr	Gln	Val	Thr	Phe	Tyr	Arg	Asp	Gly	Ser	Ala	Leu	Gly
				110					115					120
Pro	Pro	Gly	Pro	Asn	Arg	Glu	Phe	Ser	Ile	Thr	Val	Val	Gln	Lys
				125					130					135
Ala	Asp	Ser	Gly	His	Tyr	His	Cys	Ser	Gly	Ile	Phe	Gln	Ser	Pro
				140					145					150



Gly	Pro	Gly	Ile	Pro	Glu	Thr	Ala	Ser	Val	Val	Ala	Ile	Thr	Val	155	160	165
Gln	Glu	Leu	Phe	Pro	Ala	Pro	Ile	Leu	Arg	Ala	Val	Pro	Ser	Ala	170	175	180
Glu	Pro	Gln	Ala	Gly	Ser	Pro	Met	Thr	Leu	Ser	Cys	Gln	Thr	Lys	185	190	195
Leu	Pro	Leu	Gln	Arg	Ser	Ala	Ala	Arg	Leu	Leu	Phe	Ser	Phe	Tyr	200	205	210
Lys	Asp	Gly	Arg	Ile	Val	Gln	Ser	Arg	Gly	Leu	Ser	Ser	Glu	Phe	215	220	225
Gln	Ile	Pro	Thr	Ala	Ser	Glu	Asp	His	Ser	Gly	Ser	Tyr	Trp	Cys	230	235	240
Glu	Ala	Ala	Thr	Glu	Asp	Asn	Gln	Val	Trp	Lys	Gln	Ser	Pro	Gln	245	250	255
Leu	Glu	Ile	Arg	Val	Gln	Gly	Ala	Ser	Ser	Ser	Ala	Ala	Pro	Pro	260	265	270
Thr	Leu	Asn	Pro	Ala	Pro	Gln	Lys	Ser	Ala	Ala	Pro	Gly	Thr	Ala	275	280	285
Pro	Glu	Glu	Ala	Pro	Gly	Pro	Leu	Pro	Pro	Pro	Pro	Thr	Pro	Ser	290	295	300
Ser	Glu	Asp	Pro	Gly	Phe	Ser	Ser	Pro	Leu	Gly	Met	Pro	Asp	Pro	305	310	315
His	Leu	Tyr	His	Gln	Met	Gly	Leu	Leu	Leu	Lys	His	Met	Gln	Asp	320	325	330
Val	Arg	Val	Leu	Leu	Gly	His	Leu	Leu	Met	Glu	Leu	Arg	Glu	Leu	335	340	345
Ser	Gly	His	Gln	Lys	Pro	Gly	Thr	Thr	Lys	Ala	Thr	Ala	Glu		350	355	

<210> 46

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 46

tggtgtgtgt cctcatgg 18

<210> 47

<211> 18

<212> DNA

<213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 47  
 tttccagcgc caattctc 18

<210> 48  
 <211> 23  
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 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 48  
 agttcttgga ctgtgatagc cac 23

<210> 49  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 49  
 aaacttggtt gtcctcagtg gctg 24

<210> 50  
 <211> 45  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 50  
 gtgagggacc tgtctgcact gaggagagca gctgccacac ggagg 45

<210> 51  
 <211> 2181  
 <212> DNA  
 <213> Homo sapiens

<400> 51  
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 ccaccagaag tttgagcctc tttggtagca ggaggctgga agaaaggaca 100  
 gaagtagctc tggctgtgat ggggatctta ctgggcctgc tactcctggg 150  
 gcacctaaca gtggacactt atggccgtcc catcctggaa gtgccagaga 200  
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<210> 52

<211> 321

<212> PRT

<213> Homo sapiens

<400> 52

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Asp	Thr	Tyr	Gly	Arg	Pro	Ile	Leu	Glu	Val	Pro	Glu	Ser	Val	Thr
				20					25					30
Gly	Pro	Trp	Lys	Gly	Asp	Val	Asn	Leu	Pro	Cys	Thr	Tyr	Asp	Pro
				35					40					45
Leu	Gln	Gly	Tyr	Thr	Gln	Val	Leu	Val	Lys	Trp	Leu	Val	Gln	Arg
				50					55					60
Gly	Ser	Asp	Pro	Val	Thr	Ile	Phe	Leu	Arg	Asp	Ser	Ser	Gly	Asp
				65					70					75
His	Ile	Gln	Gln	Ala	Lys	Tyr	Gln	Gly	Arg	Leu	His	Val	Ser	His
				80					85					90
Lys	Val	Pro	Gly	Asp	Val	Ser	Leu	Gln	Leu	Ser	Thr	Leu	Glu	Met
				95					100					105
Asp	Asp	Arg	Ser	His	Tyr	Thr	Cys	Glu	Val	Thr	Trp	Gln	Thr	Pro
				110					115					120
Asp	Gly	Asn	Gln	Val	Val	Arg	Asp	Lys	Ile	Thr	Glu	Leu	Arg	Val
				125					130					135
Gln	Lys	Leu	Ser	Val	Ser	Lys	Pro	Thr	Val	Thr	Thr	Gly	Ser	Gly
				140					145					150
Tyr	Gly	Phe	Thr	Val	Pro	Gln	Gly	Met	Arg	Ile	Ser	Leu	Gln	Cys
				155					160					165
Gln	Ala	Arg	Gly	Ser	Pro	Pro	Ile	Ser	Tyr	Ile	Trp	Tyr	Lys	Gln
				170					175					180



<223> Synthetic oligonucleotide probe

<400> 55

cttcacaatg togctgtgct gctc 24

<210> 56

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 56

agccaaatcc agcagctggc ttac 24

<210> 57

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 57

tggatgaccg gagccactac acgtgtgaag tcacctggca gactcctgat 50

<210> 58

<211> 2458

<212> DNA

<213> Homo sapiens

<400> 58

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ccttctcctc ttgctagttt cctactatgt tggaaccttg gggactcaca 250

ctgagatcaa gagagtggca gaggaaaagg tcactttgcc ctgccaccat 300

caactggggc ttccagaaaa agacactctg gatattgaat ggctgctcac 350

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Pro	Lys	Ser	Arg	Ile	Asp	Tyr	Asn	His	Pro	Gly	Arg	Val	Leu	Leu	185	190	195
Gln	Asn	Leu	Thr	Met	Ser	Tyr	Ser	Gly	Leu	Tyr	Gln	Cys	Thr	Ala	200	205	210
Gly	Asn	Glu	Ala	Gly	Lys	Glu	Ser	Cys	Val	Val	Arg	Val	Thr	Val	215	220	225
Gln	Tyr	Val	Gln	Ser	Ile	Gly	Met	Val	Ala	Gly	Ala	Val	Thr	Gly	230	235	240
Ile	Val	Ala	Gly	Ala	Leu	Leu	Ile	Phe	Leu	Leu	Val	Trp	Leu	Leu	245	250	255
Ile	Arg	Arg	Lys	Asp	Lys	Glu	Arg	Tyr	Glu	Glu	Glu	Glu	Arg	Pro	260	265	270
Asn	Glu	Ile	Arg	Glu	Asp	Ala	Glu	Ala	Pro	Lys	Ala	Arg	Leu	Val	275	280	285
Lys	Pro	Ser	Ser	Ser	Ser	Ser	Gly	Ser	Arg	Ser	Ser	Arg	Ser	Gly	290	295	300
Ser	Ser	Ser	Thr	Arg	Ser	Thr	Ala	Asn	Ser	Ala	Ser	Arg	Ser	Gln	305	310	315
Arg	Thr	Leu	Ser	Thr	Asp	Ala	Ala	Pro	Gln	Pro	Gly	Leu	Ala	Thr	320	325	330
Gln	Ala	Tyr	Ser	Leu	Val	Gly	Pro	Glu	Val	Arg	Gly	Ser	Glu	Pro	335	340	345
Lys	Lys	Val	His	His	Ala	Asn	Leu	Thr	Lys	Ala	Glu	Thr	Thr	Pro	350	355	360
Ser	Met	Ile	Pro	Ser	Gln	Ser	Arg	Ala	Phe	Gln	Thr	Val			365	370	

<210> 60

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 60

ccagtgcaca gcaggcaacg aagc 24

<210> 61

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 61  
actaggctgt atgcctgggt gggc 24

<210> 62  
<211> 43  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 62  
gtatgtacaa agcatcggca tggttgcagg agcagtgaca ggc 43

<210> 63  
<211> 3534  
<212> DNA  
<213> Homo sapiens

<400> 63  
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<210> 64

<211> 655

<212> PRT

<213> Homo sapiens

<400> 64

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			20					25					30	

Leu	Leu	Leu	Gly	Phe	Leu	Ser	Thr	Thr	Thr	Ala	Gln	Pro	Glu	Gln	35	40	45
Lys	Ala	Ser	Asn	Leu	Ile	Gly	Thr	Tyr	Arg	His	Val	Asp	Arg	Ala	50	55	60
Thr	Gly	Gln	Val	Leu	Thr	Cys	Asp	Lys	Cys	Pro	Ala	Gly	Thr	Tyr	65	70	75
Val	Ser	Glu	His	Cys	Thr	Asn	Thr	Ser	Leu	Arg	Val	Cys	Ser	Ser	80	85	90
Cys	Pro	Val	Gly	Thr	Phe	Thr	Arg	His	Glu	Asn	Gly	Ile	Glu	Lys	95	100	105
Cys	His	Asp	Cys	Ser	Gln	Pro	Cys	Pro	Trp	Pro	Met	Ile	Glu	Lys	110	115	120
Leu	Pro	Cys	Ala	Ala	Leu	Thr	Asp	Arg	Glu	Cys	Thr	Cys	Pro	Pro	125	130	135
Gly	Met	Phe	Gln	Ser	Asn	Ala	Thr	Cys	Ala	Pro	His	Thr	Val	Cys	140	145	150
Pro	Val	Gly	Trp	Gly	Val	Arg	Lys	Lys	Gly	Thr	Glu	Thr	Glu	Asp	155	160	165
Val	Arg	Cys	Lys	Gln	Cys	Ala	Arg	Gly	Thr	Phe	Ser	Asp	Val	Pro	170	175	180
Ser	Ser	Val	Met	Lys	Cys	Lys	Ala	Tyr	Thr	Asp	Cys	Leu	Ser	Gln	185	190	195
Asn	Leu	Val	Val	Ile	Lys	Pro	Gly	Thr	Lys	Glu	Thr	Asp	Asn	Val	200	205	210
Cys	Gly	Thr	Leu	Pro	Ser	Phe	Ser	Ser	Ser	Thr	Ser	Pro	Ser	Pro	215	220	225
Gly	Thr	Ala	Ile	Phe	Pro	Arg	Pro	Glu	His	Met	Glu	Thr	His	Glu	230	235	240
Val	Pro	Ser	Ser	Thr	Tyr	Val	Pro	Lys	Gly	Met	Asn	Ser	Thr	Glu	245	250	255
Ser	Asn	Ser	Ser	Ala	Ser	Val	Arg	Pro	Lys	Val	Leu	Ser	Ser	Ile	260	265	270
Gln	Glu	Gly	Thr	Val	Pro	Asp	Asn	Thr	Ser	Ser	Ala	Arg	Gly	Lys	275	280	285
Glu	Asp	Val	Asn	Lys	Thr	Leu	Pro	Asn	Leu	Gln	Val	Val	Asn	His	290	295	300
Gln	Gln	Gly	Pro	His	His	Arg	His	Ile	Leu	Lys	Leu	Leu	Pro	Ser	305	310	315
Met	Glu	Ala	Thr	Gly	Gly	Glu	Lys	Ser	Ser	Thr	Pro	Ile	Lys	Gly			

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Pro Lys Arg Gly His 335	Pro Arg Gln Asn Leu His Lys His Phe 340	Asp 345
Ile Asn Glu His 350	Leu Pro Trp Met Ile Val Leu Phe Leu Leu Leu 355	360
Val Leu Val Val Ile Val Val Cys Ser 365	Ile Arg Lys Ser Ser Arg 370	375
Thr Leu Lys Lys Gly Pro Arg Gln Asp 380	Pro Ser Ala Ile Val Glu 385	390
Lys Ala Gly Leu Lys Lys Ser Met Thr 395	Pro Thr Gln Asn Arg Glu 400	405
Lys Trp Ile Tyr Tyr Cys Asn Gly His 410	Gly Ile Asp Ile Leu Lys 415	420
Leu Val Ala Ala Gln Val Gly Ser Gln 425	Trp Lys Asp Ile Tyr Gln 430	435
Phe Leu Cys Asn Ala Ser Glu Arg Glu 440	Val Ala Ala Phe Ser Asn 445	450
Gly Tyr Thr Ala Asp His Glu Arg Ala 455	Tyr Ala Ala Leu Gln His 460	465
Trp Thr Ile Arg Gly Pro Glu Ala Ser 470	Leu Ala Gln Leu Ile Ser 475	480
Ala Leu Arg Gln His Arg Arg Asn Asp 485	Val Val Glu Lys Ile Arg 490	495
Gly Leu Met Glu Asp Thr Thr Gln Leu 500	Glu Thr Asp Lys Leu Ala 505	510
Leu Pro Met Ser Pro Ser Pro Leu Ser 515	Pro Ser Pro Ile Pro Ser 520	525
Pro Asn Ala Lys Leu Glu Asn Ser Ala 530	Leu Leu Thr Val Glu Pro 535	540
Ser Pro Gln Asp Lys Asn Lys Gly Phe 545	Phe Val Asp Glu Ser Glu 550	555
Pro Leu Leu Arg Cys Asp Ser Thr Ser 560	Ser Gly Ser Ser Ala Leu 565	570
Ser Arg Asn Gly Ser Phe Ile Thr Lys 575	Glu Lys Lys Asp Thr Val 580	585
Leu Arg Gln Val Arg Leu Asp Pro Cys 590	Asp Leu Gln Pro Ile Phe 595	600
Asp Asp Met Leu His Phe Leu Asn Pro 605	Glu Glu Leu Arg Val Ile 610	615



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<210> 69

<211> 453

<212> PRT

<213> Homo sapiens

<400> 69

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Pro	Asp	Ala	Asp	Ala	Val	Ala	Ala	Gln	Ile	Leu	Ser	Leu	Leu	Pro
				35					40					45
Leu	Lys	Phe	Phe	Pro	Ile	Ile	Val	Ile	Gly	Ile	Ile	Ala	Leu	Ile
				50					55					60
Leu	Ala	Leu	Ala	Ile	Gly	Leu	Gly	Ile	His	Phe	Asp	Cys	Ser	Gly
				65					70					75
Lys	Tyr	Arg	Cys	Arg	Ser	Ser	Phe	Lys	Cys	Ile	Glu	Leu	Ile	Ala
				80					85					90
Arg	Cys	Asp	Gly	Val	Ser	Asp	Cys	Lys	Asp	Gly	Glu	Asp	Glu	Tyr
				95					100					105
Arg	Cys	Val	Arg	Val	Gly	Gly	Gln	Asn	Ala	Val	Leu	Gln	Val	Phe

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His Tyr Ala Asn	Val Ala Cys Ala Gln	Leu Gly Phe Pro Ser Tyr			
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Val Ser Ser Asp	Asn Leu Arg Val Ser	Ser Leu Glu Gly Gln Phe			
	155	160			165
Arg Glu Glu Phe	Val Ser Ile Asp His	Leu Leu Pro Asp Asp Lys			
	170	175			180
Val Thr Ala Leu	His His Ser Val Tyr	Val Arg Glu Gly Cys Ala			
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Ser Gly His Val	Val Thr Leu Gln Cys	Thr Ala Cys Gly His Arg			
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Arg Gly Tyr Ser	Ser Arg Ile Val Gly	Gly Asn Met Ser Leu Leu			
	215	220			225
Ser Gln Trp Pro	Trp Gln Ala Ser Leu	Gln Phe Gln Gly Tyr His			
	230	235			240
Leu Cys Gly Gly	Ser Val Ile Thr Pro	Leu Trp Ile Ile Thr Ala			
	245	250			255
Ala His Cys Val	Tyr Asp Leu Tyr Leu	Pro Lys Ser Trp Thr Ile			
	260	265			270
Gln Val Gly Leu	Val Ser Leu Leu Asp	Asn Pro Ala Pro Ser His			
	275	280			285
Leu Val Glu Lys	Ile Val Tyr His Ser	Lys Tyr Lys Pro Lys Arg			
	290	295			300
Leu Gly Asn Asp	Ile Ala Leu Met Lys	Leu Ala Gly Pro Leu Thr			
	305	310			315
Phe Asn Glu Met	Ile Gln Pro Val Cys	Leu Pro Asn Ser Glu Glu			
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Asn Phe Pro Asp	Gly Lys Val Cys Trp	Thr Ser Gly Trp Gly Ala			
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Thr Glu Asp Gly	Gly Asp Ala Ser Pro	Val Leu Asn His Ala Ala			
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Val Pro Leu Ile	Ser Asn Lys Ile Cys	Asn His Arg Asp Val Tyr			
	365	370			375
Gly Gly Ile Ile	Ser Pro Ser Met Leu	Cys Ala Gly Tyr Leu Thr			
	380	385			390
Gly Gly Val Asp	Ser Cys Gln Gly Asp	Ser Gly Gly Pro Leu Val			
	395	400			405

Cys Gln Glu Arg Arg Leu Trp Lys Leu Val Gly Ala Thr Ser Phe  
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<210> 71  
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<400> 71  
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<210> 72  
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<210> 73  
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<212> DNA  
<213> Homo sapiens

<400> 73  
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Lys	Tyr	Val	Glu	Leu	Val	Ile	Val	Ala	Asp	Asn	Arg	Glu	Phe	Gln	215	220	225
Arg	Gln	Gly	Lys	Asp	Leu	Glu	Lys	Val	Lys	Gln	Arg	Leu	Ile	Glu	230	235	240
Ile	Ala	Asn	His	Val	Asp	Lys	Phe	Tyr	Arg	Pro	Leu	Asn	Ile	Arg	245	250	255
Ile	Val	Leu	Val	Gly	Val	Glu	Val	Trp	Asn	Asp	Met	Asp	Lys	Cys	260	265	270
Ser	Val	Ser	Gln	Asp	Pro	Phe	Thr	Ser	Leu	His	Glu	Phe	Leu	Asp	275	280	285
Trp	Arg	Lys	Met	Lys	Leu	Leu	Pro	Arg	Lys	Ser	His	Asp	Asn	Ala	290	295	300
Gln	Leu	Val	Ser	Gly	Val	Tyr	Phe	Gln	Gly	Thr	Thr	Ile	Gly	Met	305	310	315
Ala	Pro	Ile	Met	Ser	Met	Cys	Thr	Ala	Asp	Gln	Ser	Gly	Gly	Ile	320	325	330
Val	Met	Asp	His	Ser	Asp	Asn	Pro	Leu	Gly	Ala	Ala	Val	Thr	Leu	335	340	345
Ala	His	Glu	Leu	Gly	His	Asn	Phe	Gly	Met	Asn	His	Asp	Thr	Leu	350	355	360
Asp	Arg	Gly	Cys	Ser	Cys	Gln	Met	Ala	Val	Glu	Lys	Gly	Gly	Cys	365	370	375
Ile	Met	Asn	Ala	Ser	Thr	Gly	Tyr	Pro	Phe	Pro	Met	Val	Phe	Ser	380	385	390
Ser	Cys	Ser	Arg	Lys	Asp	Leu	Glu	Thr	Ser	Leu	Glu	Lys	Gly	Met	395	400	405
Gly	Val	Cys	Leu	Phe	Asn	Leu	Pro	Glu	Val	Arg	Glu	Ser	Phe	Gly	410	415	420
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Asp	Cys	Gly	Glu	Pro	Glu	Glu	Cys	Met	Asn	Arg	Cys	Cys	Asn	Ala	440	445	450
Thr	Thr	Cys	Thr	Leu	Lys	Pro	Asp	Ala	Val	Cys	Ala	His	Gly	Leu	455	460	465
Cys	Cys	Glu	Asp	Cys	Gln	Leu	Lys	Pro	Ala	Gly	Thr	Ala	Cys	Arg	470	475	480
Asp	Ser	Ser	Asn	Ser	Cys	Asp	Leu	Pro	Glu	Phe	Cys	Thr	Gly	Ala	485	490	495
Ser	Pro	His	Cys	Pro	Ala	Asn	Val	Tyr	Leu	His	Asp	Gly	His	Ser			

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Cys Gln Asp Val	Asp Gly Tyr Cys Tyr	Asn Gly Ile Cys Gln Thr			
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His Glu Gln Gln	Cys Val Thr Leu Trp	Gly Pro Gly Ala Lys Pro			
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Ala Pro Gly Ile	Cys Phe Glu Arg Val	Asn Ser Ala Gly Asp Pro			
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Tyr Gly Asn Cys	Gly Lys Val Ser Lys	Ser Ser Phe Ala Lys Cys			
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Glu Met Arg Asp	Ala Lys Cys Gly Lys	Ile Gln Cys Gln Gly Gly			
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Ala Ser Arg Pro	Val Ile Gly Thr Asn	Ala Val Ser Ile Glu Thr			
	590	595			600
Asn Ile Pro Leu	Gln Gln Gly Gly Arg	Ile Leu Cys Arg Gly Thr			
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His Val Tyr Leu	Gly Asp Asp Met Pro	Asp Pro Gly Leu Val Leu			
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Ala Gly Thr Lys	Cys Ala Asp Gly Lys	Ile Cys Leu Asn Arg Gln			
	635	640			645
Cys Gln Asn Ile	Ser Val Phe Gly Val	His Glu Cys Ala Met Gln			
	650	655			660
Cys His Gly Arg	Gly Val Cys Asn Asn	Arg Lys Asn Cys His Cys			
	665	670			675
Glu Ala His Trp	Ala Pro Pro Phe Cys	Asp Lys Phe Gly Phe Gly			
	680	685			690
Gly Ser Thr Asp	Ser Gly Pro Ile Arg	Gln Ala Glu Ala Arg Gln			
	695	700			705
Glu Ala Ala Glu	Ser Asn Arg Glu Arg	Gly Gln Gly Gln Glu Pro			
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<211> 483

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 30, 94, 143, 156, 163, 179, 193, 369, 371, 381, 390, 473

<223> unknown base

<400> 75



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<210> 89  
<211> 2956  
<212> DNA  
<213> Homo sapiens

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 <212> PRT  
 <213> Homo sapiens

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 Gly Gly Arg Trp Gly Ala Arg Ala Gln Glu Ala Ala Ala Ala Ala  
 35 40 45  
 Ala Asp Gly Pro Pro Ala Ala Asp Gly Glu Asp Gly Gln Asp Pro  
 50 55 60  
 His Ser Lys His Leu Tyr Thr Ala Asp Met Phe Thr His Gly Ile  
 65 70 75  
 Gln Ser Ala Ala His Phe Val Met Phe Phe Ala Pro Trp Cys Gly  
 80 85 90  
 His Cys Gln Arg Leu Gln Pro Thr Trp Asn Asp Leu Gly Asp Lys  
 95 100 105  
 Tyr Asn Ser Met Glu Asp Ala Lys Val Tyr Val Ala Lys Val Asp  
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 Cys Thr Ala His Ser Asp Val Cys Ser Ala Gln Gly Val Arg Gly  
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 Tyr Pro Thr Leu Lys Leu Phe Lys Pro Gly Gln Glu Ala Val Lys  
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 155 160 165  
 Gln Thr Leu Asn Glu Glu Pro Val Thr Pro Glu Pro Glu Val Glu  
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Pro	Pro	Ser	Ala	Pro	Glu	Leu	Lys	Gln	Gly	Leu	Tyr	Glu	Leu	Ser	185	190	195
Ala	Ser	Asn	Phe	Glu	Leu	His	Val	Ala	Gln	Gly	Asp	His	Phe	Ile	200	205	210
Lys	Phe	Phe	Ala	Pro	Trp	Cys	Gly	His	Cys	Lys	Ala	Leu	Ala	Pro	215	220	225
Thr	Trp	Glu	Gln	Leu	Ala	Leu	Gly	Leu	Glu	His	Ser	Glu	Thr	Val	230	235	240
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Gly	Asn	Gln	Val	Arg	Gly	Tyr	Pro	Thr	Leu	Leu	Trp	Phe	Arg	Asp	260	265	270
Gly	Lys	Lys	Val	Asp	Gln	Tyr	Lys	Gly	Lys	Arg	Asp	Leu	Glu	Ser	275	280	285
Leu	Arg	Glu	Tyr	Val	Glu	Ser	Gln	Leu	Gln	Arg	Thr	Glu	Thr	Gly	290	295	300
Ala	Thr	Glu	Thr	Val	Thr	Pro	Ser	Glu	Ala	Pro	Val	Leu	Ala	Ala	305	310	315
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Asn	Phe	Asp	Asp	Thr	Ile	Ala	Glu	Gly	Ile	Thr	Phe	Ile	Lys	Phe	335	340	345
Tyr	Ala	Pro	Trp	Cys	Gly	His	Cys	Lys	Thr	Leu	Ala	Pro	Thr	Trp	350	355	360
Glu	Glu	Leu	Ser	Lys	Lys	Glu	Phe	Pro	Gly	Leu	Ala	Gly	Val	Lys	365	370	375
Ile	Ala	Glu	Val	Asp	Cys	Thr	Ala	Glu	Arg	Asn	Ile	Cys	Ser	Lys	380	385	390
Tyr	Ser	Val	Arg	Gly	Tyr	Pro	Thr	Leu	Leu	Leu	Phe	Arg	Gly	Gly	395	400	405
Lys	Lys	Val	Ser	Glu	His	Ser	Gly	Gly	Arg	Asp	Leu	Asp	Ser	Leu	410	415	420
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<210> 91

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe



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<400> 91
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<210> 92
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<220>
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<400> 92
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<210> 93
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 93
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<210> 94
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 94
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<210> 95
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<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

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<210> 96
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<212> DNA
<213> Homo sapiens

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  gtctggatat tgatagccgt cctaccgctg aagtctgtgc cacacacaca 150

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<210> 97  
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<212> PRT  
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Pro Gly Pro Lys Gly Asp Asp Gly Glu Lys Gly Asp Pro Gly Glu  
50 55 60  
Glu Gly Lys His Gly Lys Val Gly Arg Met Gly Pro Lys Gly Ile  
65 70 75  
Lys Gly Glu Leu Gly Asp Met Gly Asp Gln Gly Asn Ile Gly Lys

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Thr Gly Pro Ile	Gly Lys Lys Gly Asp	Lys Gly Glu Lys Gly	Leu
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Leu Gly Ile Pro	Gly Glu Lys Gly Lys	Ala Gly Thr Val Cys	Asp
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Cys Gly Arg Tyr	Arg Lys Phe Val Gly	Gln Leu Asp Ile Ser	Ile
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Ala Arg Leu Lys	Thr Ser Met Lys Phe	Val Lys Asn Val Ile	Ala
	140	145	150
Gly Ile Arg Glu	Thr Glu Glu Lys Phe	Tyr Tyr Ile Val Gln	Glu
	155	160	165
Glu Lys Asn Tyr	Arg Glu Ser Leu Thr	His Cys Arg Ile Arg	Gly
	170	175	180
Gly Met Leu Ala	Met Pro Lys Asp Glu	Ala Ala Asn Thr Leu	Ile
	185	190	195
Ala Asp Tyr Val	Ala Lys Ser Gly Phe	Phe Arg Val Phe Ile	Gly
	200	205	210
Val Asn Asp Leu	Glu Arg Glu Gly Gln	Tyr Met Ser Thr Asp	Asn
	215	220	225
Thr Pro Leu Gln	Asn Tyr Ser Asn Trp	Asn Glu Gly Glu Pro	Ser
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Asp Pro Tyr Gly	His Glu Asp Cys Val	Glu Met Leu Ser Ser	Gly
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<210> 98

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 98

cgctgactat gttgccaaga gtgg 24

<210> 99

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 99

gatgatggag gctccataacc tcag 24

<210> 100

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 100

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<210> 101

<211> 2574

<212> DNA

<213> Homo sapiens

<400> 101

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gagaagtctc agctagaacg agcggcccta ggttttcgga agggaggatc 200

agggatgttt gcgagcggct ggaaccagac ggtgccgata gaggaagcgg 250

gctccatggc tgccctcctg ctgctgcccc tgetgctgtt gctaccgctg 300

ctgctgctga agctacacct ctggccgcag ttgcgctggc ttccggcgga 350

cttggccttt gcggtgcgag ctctgtgctg caaaagggct cttcgagctc 400

gcgccctggc cgcggctgcc gccgaccgg aaggtccga ggggggctgc 450

agcctggcct gggcctcgc ggaactggcc cagcagcgc ccgcgcacac 500

ctttctcatt cacggctcgc ggcgcttttag ctactcagag gcggagcgcg 550

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 <212> PRT  
 <213> Homo sapiens

<400> 102  
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 20 25 30  
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 35 40 45  
 Gly Ser Met Ala Ala Leu Leu Leu Leu Pro Leu Leu Leu Leu Leu  
 50 55 60  
 Pro Leu Leu Leu Leu Lys Leu His Leu Trp Pro Gln Leu Arg Trp  
 65 70 75  
 Leu Pro Ala Asp Leu Ala Phe Ala Val Arg Ala Leu Cys Cys Lys  
 80 85 90  
 Arg Ala Leu Arg Ala Arg Ala Leu Ala Ala Ala Ala Asp Pro  
 95 100 105  
 Glu Gly Pro Glu Gly Gly Cys Ser Leu Ala Trp Arg Leu Ala Glu  
 110 115 120  
 Leu Ala Gln Gln Arg Ala Ala His Thr Phe Leu Ile His Gly Ser  
 125 130 135  
 Arg Arg Phe Ser Tyr Ser Glu Ala Glu Arg Glu Ser Asn Arg Ala  
 140 145 150  
 Ala Arg Ala Phe Leu Arg Ala Leu Gly Trp Asp Trp Gly Pro Asp  
 155 160 165  
 Gly Gly Asp Ser Gly Glu Gly Ser Ala Gly Glu Gly Glu Arg Ala  
 170 175 180  
 Ala Pro Gly Ala Gly Asp Ala Ala Ala Gly Ser Gly Ala Glu Phe  
 185 190 195  
 Ala Gly Gly Asp Gly Ala Ala Arg Gly Gly Gly Ala Ala Ala Pro  
 200 205 210

1007001-1007001

Leu Ser Pro Gly	Ala Thr Val Ala Leu	Leu Leu Pro Ala Gly	Pro
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Glu Phe Leu Trp	Leu Trp Phe Gly Leu	Ala Lys Ala Gly Leu	Arg
230		235	240
Thr Ala Phe Val	Pro Thr Ala Leu Arg	Arg Gly Pro Leu Leu	His
245		250	255
Cys Leu Arg Ser	Cys Gly Ala Arg Ala	Leu Val Leu Ala Pro	Glu
260		265	270
Phe Leu Glu Ser	Leu Glu Pro Asp Leu	Pro Ala Leu Arg Ala	Met
275		280	285
Gly Leu His Leu	Trp Ala Ala Gly Pro	Gly Thr His Pro Ala	Gly
290		295	300
Ile Ser Asp Leu	Leu Ala Glu Val Ser	Ala Glu Val Asp Gly	Pro
305		310	315
Val Pro Gly Tyr	Leu Ser Ser Pro Gln	Ser Ile Thr Asp Thr	Cys
320		325	330
Leu Tyr Ile Phe	Thr Ser Gly Thr Thr	Gly Leu Pro Lys Ala	Ala
335		340	345
Arg Ile Ser His	Leu Lys Ile Leu Gln	Cys Gln Gly Phe Tyr	Gln
350		355	360
Leu Cys Gly Val	His Gln Glu Asp Val	Ile Tyr Leu Ala Leu	Pro
365		370	375
Leu Tyr His Met	Ser Gly Ser Leu Leu	Gly Ile Val Gly Cys	Met
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Gly Ile Gly Ala	Thr Val Val Leu Lys	Ser Lys Phe Ser Ala	Gly
395		400	405
Gln Phe Trp Glu	Asp Cys Gln Gln His	Arg Val Thr Val Phe	Gln
410		415	420
Tyr Ile Gly Glu	Leu Cys Arg Tyr Leu	Val Asn Gln Pro Pro	Ser
425		430	435
Lys Ala Glu Arg	Gly His Lys Val Arg	Leu Ala Val Gly Ser	Gly
440		445	450
Leu Arg Pro Asp	Thr Trp Glu Arg Phe	Val Arg Arg Phe Gly	Pro
455		460	465
Leu Gln Val Leu	Glu Thr Tyr Gly Leu	Thr Glu Gly Asn Val	Ala
470		475	480
Thr Ile Asn Tyr	Thr Gly Gln Arg Gly	Ala Val Gly Arg Ala	Ser
485		490	495
Trp Leu Tyr Lys	His Ile Phe Pro Phe	Ser Leu Ile Arg Tyr	Asp

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Val Thr Thr Gly	Glu Pro Ile Arg Asp 515	Pro Gln Gly His Cys 520	Met 525
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Gln Gln Ser Pro	Phe Leu Gly Tyr Ala 545	Gly Gly Pro Glu Leu 550	Ala 555
Gln Gly Lys Leu	Leu Lys Asp Val Phe 560	Arg Pro Gly Asp Val 565	Phe 570
Phe Asn Thr Gly	Asp Leu Leu Val Cys 575	Asp Asp Gln Gly Phe 580	Leu 585
Arg Phe His Asp	Arg Thr Gly Asp Thr 590	Phe Arg Trp Lys Gly 595	Glu 600
Asn Val Ala Thr	Thr Glu Val Ala Glu 605	Val Phe Glu Ala Leu 610	Asp 615
Phe Leu Gln Glu	Val Asn Val Tyr Gly 620	Val Thr Val Pro Gly 625	His 630
Glu Gly Arg Ala	Gly Met Ala Ala Leu 635	Val Leu Arg Pro Pro 640	His 645
Ala Leu Asp Leu	Met Gln Leu Tyr Thr 650	His Val Ser Glu Asn 655	Leu 660
Pro Pro Tyr Ala	Arg Pro Arg Phe Leu 665	Arg Leu Gln Glu Ser 670	Leu 675
Ala Thr Thr Glu	Thr Phe Lys Gln Gln 680	Lys Val Arg Met Ala 685	Asn 690
Glu Gly Phe Asp	Pro Ser Thr Leu Ser 695	Asp Pro Leu Tyr Val 700	Leu 705
Asp Gln Ala Val	Gly Ala Tyr Leu Pro 710	Leu Thr Thr Ala Arg 715	Tyr 720
Ser Ala Leu Leu	Ala Gly Asn Leu Arg 725	Ile 730	

<210> 103

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 103

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<210> 104  
 <211> 18  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 104  
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<210> 105  
 <211> 26  
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 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 105  
 gccctggcac agtgactcca tagacg 26

<210> 106  
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<220>  
 <223> Synthetic oligonucleotide probe

<400> 106  
 atccacttca gcggacac 18

<210> 107  
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 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 107  
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<210> 108  
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 <212> DNA  
 <213> Homo sapiens

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Ser	Gln	Gln	Ser	Lys	Leu	Glu	Phe	Glu	Asn	Leu	Val	Glu	Glu	Thr	80	85	90
Ser	His	Phe	Val	Arg	Thr	Thr	Phe	Val	Ser	Arg	His	Lys	Lys	Phe	95	100	105
Asp	Glu	Phe	Phe	Arg	Glu	Leu	Leu	Glu	Asn	Ala	Glu	Lys	Ser	Leu	110	115	120
Asn	Asp	Met	Phe	Val	Arg	Thr	Tyr	Gly	Met	Leu	Tyr	Met	Gln	Asn	125	130	135
Ser	Glu	Val	Phe	Gln	Asp	Leu	Phe	Thr	Glu	Leu	Lys	Arg	Tyr	Tyr	140	145	150
Thr	Gly	Gly	Asn	Val	Asn	Leu	Glu	Glu	Met	Leu	Asn	Asp	Phe	Trp	155	160	165
Ala	Arg	Leu	Leu	Glu	Arg	Met	Phe	Gln	Leu	Ile	Asn	Pro	Gln	Tyr	170	175	180
His	Phe	Ser	Glu	Asp	Tyr	Leu	Glu	Cys	Val	Ser	Lys	Tyr	Thr	Asp	185	190	195
Gln	Leu	Lys	Pro	Phe	Gly	Asp	Val	Pro	Arg	Lys	Leu	Lys	Ile	Gln	200	205	210
Val	Thr	Arg	Ala	Phe	Ile	Ala	Ala	Arg	Thr	Phe	Val	Gln	Gly	Leu	215	220	225
Thr	Val	Gly	Arg	Glu	Val	Ala	Asn	Arg	Val	Ser	Lys	Val	Ser	Pro	230	235	240
Thr	Pro	Gly	Cys	Ile	Arg	Ala	Leu	Met	Lys	Met	Leu	Tyr	Cys	Pro	245	250	255
Tyr	Cys	Arg	Gly	Leu	Pro	Thr	Val	Arg	Pro	Cys	Asn	Asn	Tyr	Cys	260	265	270
Leu	Asn	Val	Met	Lys	Gly	Cys	Leu	Ala	Asn	Gln	Ala	Asp	Leu	Asp	275	280	285
Thr	Glu	Trp	Asn	Leu	Phe	Ile	Asp	Ala	Met	Leu	Leu	Val	Ala	Glu	290	295	300
Arg	Leu	Glu	Gly	Pro	Phe	Asn	Ile	Glu	Ser	Val	Met	Asp	Pro	Ile	305	310	315
Asp	Val	Lys	Ile	Ser	Glu	Ala	Ile	Met	Asn	Met	Gln	Glu	Asn	Ser	320	325	330
Met	Gln	Val	Ser	Ala	Lys	Val	Phe	Gln	Gly	Cys	Gly	Gln	Pro	Lys	335	340	345
Pro	Ala	Pro	Ala	Leu	Arg	Ser	Ala	Arg	Ser	Ala	Pro	Glu	Asn	Phe	350	355	360
Asn	Thr	Arg	Phe	Arg	Pro	Tyr	Asn	Pro	Glu	Glu	Arg	Pro	Thr	Thr			

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Ala Ala Gly Thr	Ser Leu Asp Arg Leu	Val Thr Asp Ile Lys Glu			
	380	385			390
Lys Leu Lys Leu	Ser Lys Lys Val Trp	Ser Ala Leu Pro Tyr Thr			
	395	400			405
Ile Cys Lys Asp	Glu Ser Val Thr Ala	Gly Thr Ser Asn Glu Glu			
	410	415			420
Glu Cys Trp Asn	Gly His Ser Lys Ala	Arg Tyr Leu Pro Glu Ile			
	425	430			435
Met Asn Asp Gly	Leu Thr Asn Gln Ile	Asn Asn Pro Glu Val Asp			
	440	445			450
Val Asp Ile Thr	Arg Pro Asp Thr Phe	Ile Arg Gln Gln Ile Met			
	455	460			465
Ala Leu Arg Val	Met Thr Asn Lys Leu	Lys Asn Ala Tyr Asn Gly			
	470	475			480
Asn Asp Val Asn	Phe Gln Asp Thr Ser	Asp Glu Ser Ser Gly Ser			
	485	490			495
Gly Ser Gly Ser	Gly Cys Met Asp Asp	Val Cys Pro Thr Glu Phe			
	500	505			510
Glu Phe Val Thr	Thr Glu Ala Pro Ala	Val Asp Pro Asp Arg Arg			
	515	520			525
Glu Val Asp Ser	Ser Ala Ala Gln Arg	Gly His Ser Leu Leu Ser			
	530	535			540
Trp Ser Leu Thr	Cys Ile Val Leu Ala	Leu Gln Arg Leu Cys Arg			
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<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 110

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<210> 111

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 111

tgcacagtct ctgcagtgcc cagg 24

<210> 112

<211> 40

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 112

gaatgctgga acgggcacag caaagccaga tacttgctg 40

<210> 113

<211> 4649

<212> DNA

<213> Homo sapiens

<400> 113

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 gtgcaaaact agttgcgggt tttccatta aaagtaataa ccttactctt 3900





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Ile Cys Thr Pro	Ser Arg Ser Gln Phe	Ile Thr Gly Lys Tyr Gln			
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Ile His Thr Gly	Leu Gln His Ser Ile	Ile Arg Pro Thr Gln Pro			
	140	145			150
Asn Cys Leu Pro	Leu Asp Asn Ala Thr	Leu Pro Gln Lys Leu Lys			
	155	160			165
Glu Val Gly Tyr	Ser Thr His Met Val	Gly Lys Trp His Leu Gly			
	170	175			180
Phe Asn Arg Lys	Glu Cys Met Pro Thr	Arg Arg Gly Phe Asp Thr			
	185	190			195
Phe Phe Gly Ser	Leu Leu Gly Ser Gly	Asp Tyr Tyr Thr His Tyr			
	200	205			210
Lys Cys Asp Ser	Pro Gly Met Cys Gly	Tyr Asp Leu Tyr Glu Asn			
	215	220			225
Asp Asn Ala Ala	Trp Asp Tyr Asp Asn	Gly Ile Tyr Ser Thr Gln			
	230	235			240
Met Tyr Thr Gln	Arg Val Gln Gln Ile	Leu Ala Ser His Asn Pro			
	245	250			255
Thr Lys Pro Ile	Phe Leu Tyr Thr Ala	Tyr Gln Ala Val His Ser			
	260	265			270
Pro Leu Gln Ala	Pro Gly Arg Tyr Phe	Glu His Tyr Arg Ser Ile			
	275	280			285
Ile Asn Ile Asn	Arg Arg Arg Tyr Ala	Ala Met Leu Ser Cys Leu			
	290	295			300
Asp Glu Ala Ile	Asn Asn Val Thr Leu	Ala Leu Lys Thr Tyr Gly			
	305	310			315
Phe Tyr Asn Asn	Ser Ile Ile Ile Tyr	Ser Ser Asp Asn Gly Gly			
	320	325			330
Gln Pro Thr Ala	Gly Gly Ser Asn Trp	Pro Leu Arg Gly Ser Lys			
	335	340			345
Gly Thr Tyr Trp	Glu Gly Gly Ile Arg	Ala Val Gly Phe Val His			
	350	355			360
Ser Pro Leu Leu	Lys Asn Lys Gly Thr	Val Cys Lys Glu Leu Val			
	365	370			375
His Ile Thr Asp	Trp Tyr Pro Thr Leu	Ile Ser Leu Ala Glu Gly			
	380	385			390
Gln Ile Asp Glu	Asp Ile Gln Leu Asp	Gly Tyr Asp Ile Trp Glu			
	395	400			405



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gccaccctac ctcagaaact gaaggagggtt ggntattcaa cgcatatggt 50  
cgg 53

<210> 118  
<211> 2260  
<212> DNA  
<213> Homo sapiens

<220>  
<221> unsure  
<222> 2009, 2026, 2033, 2055, 2074, 2078, 2086  
<223> unknown base

<400> 118  
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gggctcagga ggaggaagga ggacccgtgc gagaatgcct ctgccctgga 150  
gccttgcgct cccgctgctg ctctcctggg tggcaggtgg ttctgggaac 200  
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ggtctgtcac tatggaacta aactggcctg ctgctacggc tggagaagaa 300  
acagcaaggg agtctgtgaa gctacatgcg aacctggatg taagtttggg 350  
gagtgcgtgg gaccaaaca atgcagatgc tttccaggat acaccgggaa 400  
aacctgcagt caagatgtga atgagtgtgg aatgaaaccc cggccatgcc 450  
aacacagatg tgtgaataca cacggaagct acaagtgctt ttgcctcagt 500  
ggccacatgc tcatgccaga tgctacgtgt gtgaactcta ggacatgtgc 550  
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gcctgtgtcc atcctcagga ctccgcctgg ccccaaattg aagagactgt 650  
ctagatattg atgaatgtgc ctctggtaaa gtcactctgc cctacaatcg 700  
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ccaaggtgcc ttcaagtgtg aatgcaagca gggatataaa ggcaatggac 900  
ttcgggtgtc tgctatccct gaaaattctg tgaaggaagt cctcagagca 950  
cctggtacca tcaaagacag aatcaagaag ttgcttgctc aaaaaaacag 1000  
catgaaaaag aaggcaaaaa ttaaaatgt taccacagaa cccaccagga 1050





	305		310		315
Phe Asn Tyr Glu	Glu Ile Val Ser Arg	Gly Gly Asn Ser His	Gly		
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Gly Lys Lys Gly	Asn Glu Glu Lys				
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 <211> 22  
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<220>  
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<210> 121  
 <211> 24  
 <212> DNA  
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<220>  
 <223> Synthetic oligonucleotide probe

<400> 121  
 ggctgcacgt atggctatcc atag 24

<210> 122  
 <211> 50  
 <212> DNA  
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<220>  
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<400> 122  
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<210> 123  
 <211> 1199  
 <212> DNA  
 <213> Homo sapiens

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 ggccgagtgg cagggacgac gcccagaatg ggagctgact gatatggtgg 150  
 tgtgggtgac tggagcctcg agtgggaattg gtgaggagct ggcttaccag 200  
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 gctggaaagg gtgaaaagaa gatgcctaga gaatggcaat ttaaaagaaa 300





	80	85	90
Met Ser Gln Arg	Ser Leu Cys Met Asp	Thr Ser Leu Asp Val	Tyr
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Arg Lys Leu Ile	Glu Leu Asn Tyr Leu	Gly Thr Val Ser Leu	Thr
	110	115	120
Lys Cys Val Leu	Pro His Met Ile Glu	Arg Lys Gln Gly Lys	Ile
	125	130	135
Val Thr Val Asn	Ser Ile Leu Gly Ile	Ile Ser Val Pro Leu	Ser
	140	145	150
Ile Gly Tyr Cys	Ala Ser Lys His Ala	Leu Arg Gly Phe Phe	Asn
	155	160	165
Gly Leu Arg Thr	Glu Leu Ala Thr Tyr	Pro Gly Ile Ile Val	Ser
	170	175	180
Asn Ile Cys Pro	Gly Pro Val Gln Ser	Asn Ile Val Glu Asn	Ser
	185	190	195
Leu Ala Gly Glu	Val Thr Lys Thr Ile	Gly Asn Asn Gly Asp	Gln
	200	205	210
Ser His Lys Met	Thr Thr Ser Arg Cys	Val Arg Leu Met Leu	Ile
	215	220	225
Ser Met Ala Asn	Asp Leu Lys Glu Val	Trp Ile Ser Glu Gln	Pro
	230	235	240
Phe Leu Leu Val	Thr Tyr Leu Trp Gln	Tyr Met Pro Thr Trp	Ala
	245	250	255
Trp Trp Ile Thr	Asn Lys Met Gly Lys	Lys Arg Ile Glu Asn	Phe
	260	265	270
Lys Ser Gly Val	Asp Ala Asp Ser Ser	Tyr Phe Lys Ile Phe	Lys
	275	280	285
Thr Lys His Asp			

<210> 125

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 125

gcaatgaact gggagctgc 19

<210> 126

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 126

ctgtgaatag catcctggg 19

<210> 127

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 127

cttttcaagc cactggaggg 20

<210> 128

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 128

ctgtagacat ccaagctggg atcc 24

<210> 129

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 129

aagagtctgc atccacacca ctc 23

<210> 130

<211> 46

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 130

acctgacgct actatgggcc gagtggcagg gacgacgccc agaattg 46

<210> 131

<211> 2365

<212> DNA

<213> Homo sapiens

<400> 131



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<210> 132  
 <211> 571  
 <212> PRT  
 <213> Homo sapiens

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 Ile Thr Thr Tyr Ala Ile Asn Val Ser Leu Met Trp Leu Ser Phe  
 35 40 45  
 Arg Lys Val Gln Glu Pro Gln Gly Lys Ala Lys Arg His Gly Asn  
 50 55 60  
 Thr Val Pro Gly Glu Trp Pro Trp Gln Ala Ser Val Arg Arg Gln  
 65 70 75

Gly	Ala	His	Ile	Cys	Ser	Gly	Ser	Leu	Val	Ala	Asp	Thr	Trp	Val	
				80					85					90	
Leu	Thr	Ala	Ala	His	Cys	Phe	Glu	Lys	Ala	Ala	Ala	Thr	Glu	Leu	
				95					100					105	
Asn	Ser	Trp	Ser	Val	Val	Leu	Gly	Ser	Leu	Gln	Arg	Glu	Gly	Leu	
				110					115					120	
Ser	Pro	Gly	Ala	Glu	Glu	Val	Gly	Val	Ala	Ala	Leu	Gln	Leu	Pro	
				125					130					135	
Arg	Ala	Tyr	Asn	His	Tyr	Ser	Gln	Gly	Ser	Asp	Leu	Ala	Leu	Leu	
				140					145					150	
Gln	Leu	Ala	His	Pro	Thr	Thr	His	Thr	Pro	Leu	Cys	Leu	Pro	Gln	
				155					160					165	
Pro	Ala	His	Arg	Phe	Pro	Phe	Gly	Ala	Ser	Cys	Trp	Ala	Thr	Gly	
				170					175					180	
Trp	Asp	Gln	Asp	Thr	Ser	Asp	Ala	Pro	Gly	Thr	Leu	Arg	Asn	Leu	
				185					190					195	
Arg	Leu	Arg	Leu	Ile	Ser	Arg	Pro	Thr	Cys	Asn	Cys	Ile	Tyr	Asn	
				200					205					210	
Gln	Leu	His	Gln	Arg	His	Leu	Ser	Asn	Pro	Ala	Arg	Pro	Gly	Met	
				215					220					225	
Leu	Cys	Gly	Gly	Pro	Gln	Pro	Gly	Val	Gln	Gly	Pro	Cys	Gln	Gly	
				230					235					240	
Asp	Ser	Gly	Gly	Pro	Val	Leu	Cys	Leu	Glu	Pro	Asp	Gly	His	Trp	
				245					250					255	
Val	Gln	Ala	Gly	Ile	Ile	Ser	Phe	Ala	Ser	Ser	Cys	Ala	Gln	Glu	
				260					265					270	
Asp	Ala	Pro	Val	Leu	Leu	Thr	Asn	Thr	Ala	Ala	His	Ser	Ser	Trp	
				275					280					285	
Leu	Gln	Ala	Arg	Val	Gln	Gly	Ala	Ala	Phe	Leu	Ala	Gln	Ser	Pro	
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Glu	Thr	Pro	Glu	Met	Ser	Asp	Glu	Asp	Ser	Cys	Val	Ala	Cys	Gly	
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Ser	Leu	Arg	Thr	Ala	Gly	Pro	Gln	Ala	Gly	Ala	Pro	Ser	Pro	Trp	
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Pro	Trp	Glu	Ala	Arg	Leu	Met	His	Gln	Gly	Gln	Leu	Ala	Cys	Gly	
				335					340					345	
Gly	Ala	Leu	Val	Ser	Glu	Glu	Ala	Val	Leu	Thr	Ala	Ala	His	Cys	
				350					355					360	
Phe	Ile	Gly	Arg	Gln	Ala	Pro	Glu	Glu	Trp	Ser	Val	Gly	Leu	Gly	

				365					370					375
Thr	Arg	Pro	Glu	Glu 380	Trp	Gly	Leu	Lys	Gln 385	Leu	Ile	Leu	His	Gly 390
Ala	Tyr	Thr	His	Pro 395	Glu	Gly	Gly	Tyr	Asp 400	Met	Ala	Leu	Leu	Leu 405
Leu	Ala	Gln	Pro	Val 410	Thr	Leu	Gly	Ala	Ser 415	Leu	Arg	Pro	Leu	Cys 420
Leu	Pro	Tyr	Pro	Asp 425	His	His	Leu	Pro	Asp 430	Gly	Glu	Arg	Gly	Trp 435
Val	Leu	Gly	Arg	Ala 440	Arg	Pro	Gly	Ala	Gly 445	Ile	Ser	Ser	Leu	Gln 450
Thr	Val	Pro	Val	Thr 455	Leu	Leu	Gly	Pro	Arg 460	Ala	Cys	Ser	Arg	Leu 465
His	Ala	Ala	Pro	Gly 470	Gly	Asp	Gly	Ser	Pro 475	Ile	Leu	Pro	Gly	Met 480
Val	Cys	Thr	Ser	Ala 485	Val	Gly	Glu	Leu	Pro 490	Ser	Cys	Glu	Gly	Leu 495
Ser	Gly	Ala	Pro	Leu 500	Val	His	Glu	Val	Arg 505	Gly	Thr	Trp	Phe	Leu 510
Ala	Gly	Leu	His	Ser 515	Phe	Gly	Asp	Ala	Cys 520	Gln	Gly	Pro	Ala	Arg 525
Pro	Ala	Val	Phe	Thr 530	Ala	Leu	Pro	Ala	Tyr 535	Glu	Asp	Trp	Val	Ser 540
Ser	Leu	Asp	Trp	Gln 545	Val	Tyr	Phe	Ala	Glu 550	Glu	Pro	Glu	Pro	Glu 555
Ala	Glu	Pro	Gly	Ser 560	Cys	Leu	Ala	Asn	Ile 565	Ser	Gln	Pro	Thr	Ser 570

Cys

<210> 133

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 133

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<210> 134

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 134

gtgggcagca gttagcaccg cctc 24

<210> 135

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 135

ggctggcatc atcagctttg catcaagctg tgcccaggag gacgc 45

<210> 136

<211> 1998

<212> DNA

<213> Homo sapiens

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ggggcagcct tccaccacgg ggagcccagc tgtcagccgc ctcacaggaa 150  
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 atgccttccg gatgtcatct ctccctgcc caggaatgga agatgtgagg 1900  
 acttctaatt taaatgtggg actcggaggg attttgtaaa ctgggggtat 1950  
 attttgggga aaataaatgt ctttgtaaaa aaaaaaaaaa aaaaaaaa 1998

<210> 137

<211> 316

<212> PRT

<213> Homo sapiens

<220>

<221> unsure

<222> 233

<223> unknown amino acid

<400> 137

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Val Gln Val Pro	Glu Asp Pro Val Val	Ala Leu Val Gly Thr	Asp
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Ala Thr Leu Cys	Cys Ser Phe Ser Pro	Glu Pro Gly Phe Ser	Leu
50	55		60
Ala Gln Leu Asn	Leu Ile Trp Gln Leu	Thr Asp Thr Lys Gln	Leu
65	70		75
Val His Ser Phe	Ala Glu Gly Gln Asp	Gln Gly Ser Ala Tyr	Ala
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Asn Arg Thr Ala	Leu Phe Pro Asp Leu	Leu Ala Gln Gly Asn	Ala
95	100		105
Ser Leu Arg Leu	Gln Arg Val Arg Val	Ala Asp Glu Gly Ser	Phe
110	115		120
Thr Cys Phe Val	Ser Ile Arg Asp Phe	Gly Ser Ala Ala Val	Ser
125	130		135
Leu Gln Val Ala	Ala Pro Tyr Ser Lys	Pro Ser Met Thr Leu	Glu
140	145		150
Pro Asn Lys Asp	Leu Arg Pro Gly Asp	Thr Val Thr Ile Thr	Cys
155	160		165
Ser Ser Tyr Gln	Gly Tyr Pro Glu Ala	Glu Val Phe Trp Gln	Asp
170	175		180
Gly Gln Gly Val	Pro Leu Thr Gly Asn	Val Thr Thr Ser Gln	Met
185	190		195
Ala Asn Glu Gln	Gly Leu Phe Asp Val	His Ser Val Leu Arg	Val
200	205		210
Val Leu Gly Ala	Asn Gly Thr Tyr Ser	Cys Leu Val Arg Asn	Pro
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Val Leu Gln Gln	Asp Ala His Xaa Ser	Val Thr Ile Thr Gly	Gln
230	235		240
Pro Met Thr Phe	Pro Pro Glu Ala Leu	Trp Val Thr Val Gly	Leu
245	250		255
Ser Val Cys Leu	Ile Ala Leu Leu Val	Ala Leu Ala Phe Val	Cys
260	265		270
Trp Arg Lys Ile	Lys Gln Ser Cys Glu	Glu Glu Asn Ala Gly	Ala
275	280		285
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290	295		300

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<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 138

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<210> 139

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 139

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<210> 140

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 140

ggacacagta tactgaccac 20

<210> 141

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 141

tgccaaccag gcagctgtaa gtgc 24

<210> 142

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

10017031-103401

<400> 142  
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<210> 143  
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<220>  
 <223> Synthetic oligonucleotide probe

<400> 143  
 cagctgacag acaccaaaca gctggtgcac agtttcaccg aaggc 45

<210> 144  
 <211> 2336  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> unsure  
 <222> 1620, 1673  
 <223> unknown base

<400> 144  
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 tacgttctta aatctatgaa gtcgaggac ctttcgctgc tttttagagg 150  
 acttctttcc ttgcttcagc aacatgaggc ttttcttggtg gaacgcggtc 200  
 ttgactctgt tcgtcacttc tttgattggg gctttgatcc ctgaaccaga 250  
 agtgaaaatt gaagttctcc agaagccatt catctgccat cgcaagacca 300  
 aaggagggga tttgatgttg gtccactatg aaggctactt agaaaaggac 350  
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 gtttacccctg ggcctcctgg aggtctctcaa aggttgggac cagggcttga 450  
 aaggaatgtg tgtaggagag aagagaaagc tcatcattcc tcctgctctg 500  
 ggctatggaa aagaaggaaa aggtaaaatt cccccagaaa gtacactgat 550  
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 cattccaaga aatggatctt aatgatgact ggaaactctc taaagatgag 650  
 gttaaagcat atttaaagaa ggagtttgaa aaacatgggtg cggtggtgaa 700  
 tgaaagtcac catgatgctt tgggtggagga tatttttgat aaagaagatg 750  
 aagacaaaga tgggtttata tctgccagag aatttacata taaacacgat 800  
 gagttataga gatacatcta cccttttaat atagcactca tctttcaaga 850

gagggcagtc atctttaag aacattttat tttatacaa tgttctttct 900  
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 cccttaggtt tctaagtacc catttctttc tgataagtta ttgggaagaa 1000  
 aaagctaatt ggtctttgaa tagaagactt ctggacaatt tttcactttc 1050  
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 caactgggaa tataaccacga catgagacca ggttatagca caaattagca 1150  
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 gtctacattt toccatttct gtctcatcaa aaactgaagt tagctgggtg 2000  
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 tgtctctact aaaaatacaa aaattagcca ggcgtggtgg tgcacacctg 2150  
 tagtcccagc tactcgggag gctgagacag gagatttgct tgaaccggg 2200  
 aggcggaggt tgcagtgagc caagattgtg ccaactgcact ccagcctggg 2250  
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gcagctacta ttgaataaat acctatcctg gatttt 2336

<210> 145

<211> 211

<212> PRT

<213> Homo sapiens

<400> 145

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20 25 30

Val Leu Gln Lys Pro Phe Ile Cys His Arg Lys Thr Lys Gly Gly  
35 40 45

Asp Leu Met Leu Val His Tyr Glu Gly Tyr Leu Glu Lys Asp Gly  
50 55 60

Ser Leu Phe His Ser Thr His Lys His Asn Asn Gly Gln Pro Ile  
65 70 75

Trp Phe Thr Leu Gly Ile Leu Glu Ala Leu Lys Gly Trp Asp Gln  
80 85 90

Gly Leu Lys Gly Met Cys Val Gly Glu Lys Arg Lys Leu Ile Ile  
95 100 105

Pro Pro Ala Leu Gly Tyr Gly Lys Glu Gly Lys Gly Lys Ile Pro  
110 115 120

Pro Glu Ser Thr Leu Ile Phe Asn Ile Asp Leu Leu Glu Ile Arg  
125 130 135

Asn Gly Pro Arg Ser His Glu Ser Phe Gln Glu Met Asp Leu Asn  
140 145 150

Asp Asp Trp Lys Leu Ser Lys Asp Glu Val Lys Ala Tyr Leu Lys  
155 160 165

Lys Glu Phe Glu Lys His Gly Ala Val Val Asn Glu Ser His His  
170 175 180

Asp Ala Leu Val Glu Asp Ile Phe Asp Lys Glu Asp Glu Asp Lys  
185 190 195

Asp Gly Phe Ile Ser Ala Arg Glu Phe Thr Tyr Lys His Asp Glu  
200 205 210

Leu

<210> 146

<211> 26

<212> DNA

<213> Artificial Sequence

10017051.102401



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 caagacggac ggtgaaggca acccgatga tggcgccaag tagtgggtgg 800  
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 ctggggggag gcaggaggca catgtgaggg tccccagaga gaaggagtg 1100  
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 ggccatgttg ggccctcgtt tccattgcta gtggcctcct tggggctcct 1450  
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 tgcggccacg ctactcgctc ctctcccaac aactcccttc gtggggacaa 1900  
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 ctttgggagg ccaaggcggg tggattacct ccactgttt agtagaatg 2000  
 ggcaaaacc catctctact aaaaatacaa gaattagctg ggcgtgggtg 2050

cgtgtgcctg taatcccagc tatttgggag gctgaggcag gagaatcgct 2100  
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<210> 150  
 <211> 215  
 <212> PRT  
 <213> Homo sapiens

<400> 150  
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 Gly Leu Ser Leu Phe Phe Ser Leu Val Pro Pro Gly Arg Ser Met  
 20 25 30  
 Glu Val Thr Val Pro Ala Thr Leu Asn Val Leu Asn Gly Ser Asp  
 35 40 45  
 Ala Arg Leu Pro Cys Thr Phe Asn Ser Cys Tyr Thr Val Asn His  
 50 55 60  
 Lys Gln Phe Ser Leu Asn Trp Thr Tyr Gln Glu Cys Asn Asn Cys  
 65 70 75  
 Ser Glu Glu Met Phe Leu Gln Phe Arg Met Lys Ile Ile Asn Leu  
 80 85 90  
 Lys Leu Glu Arg Phe Gln Asp Arg Val Glu Phe Ser Gly Asn Pro  
 95 100 105  
 Ser Lys Tyr Asp Val Ser Val Met Leu Arg Asn Val Gln Pro Glu  
 110 115 120  
 Asp Glu Gly Ile Tyr Asn Cys Tyr Ile Met Asn Pro Pro Asp Arg  
 125 130 135  
 His Arg Gly His Gly Lys Ile His Leu Gln Val Leu Met Glu Glu  
 140 145 150  
 Pro Pro Glu Arg Asp Ser Thr Val Ala Val Ile Val Gly Ala Ser  
 155 160 165  
 Val Gly Gly Phe Leu Ala Val Val Ile Leu Val Leu Met Val Val  
 170 175 180  
 Lys Cys Val Arg Arg Lys Lys Glu Gln Lys Leu Ser Thr Asp Asp  
 185 190 195  
 Leu Lys Thr Glu Glu Glu Gly Lys Thr Asp Gly Glu Gly Asn Pro  
 200 205 210  
 Asp Asp Gly Ala Lys  
 215

<210> 151



<211> 524  
<212> DNA  
<213> Homo sapiens

<220>  
<221> unsure  
<222> 103, 233  
<223> unknown base

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ccnactaaca tctcagtctc tgaaaatgca cagagatgcc tggctacctc 150  
gccctgcctt cagcctcagc gggctcagtc tttttttctc tttggtgcca 200  
ccaggacgga gcatggaggt ccacagtacc tgnccaccct caacgtcctc 250  
aatggctctg acgcccgcct gccctgccct tcaactcctg ctacacagtg 300  
aaccacaaac agttctccct gaactggact taccaggagt gcaacaactg 350  
ctctgaggag atgttctctc agttccgcat gaagatcatt aacctgaagc 400  
tggagcgggt tcaagaccgc gtggagttct caggaaccc cagcaagtac 450  
gatgtgtcgg tgatgctgag aaacgtgcag ccggaggatg aggggattta 500  
caactgctac atcatgaacc cccc 524

<210> 152  
<211> 368  
<212> DNA  
<213> Homo sapiens

<220>  
<221> unsure  
<222> 56, 123  
<223> unknown base

<400> 152  
tcacgggggt catctctttt tctcttttgt gccaccagg acggagcatg 50  
gaggtncaca tacctgccac cctcaacgtc ctcaatggct ttgacgccc 100  
cctgccctgc accttcaact ccngctacac agtgaaccac aaacagttct 150  
cctgaactg gatttaccag gagtgaaca actggctctg aggagatgtt 200  
cctccagttc ccgcatggaa gatcatttaa cctgaaagct ggaagcgggt 250  
ttcaagaacc gcggtgaagt ttctcagga accccagcaa gtacgatgtg 300  
tcggtgatgc tgagaaacgt gcagccggag gatgagggga tttacaactg 350  
ctacatcatg aaccccc 368

<210> 153  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 153  
 acggagcatg gaggtccaca gtac 24

<210> 154  
 <211> 23  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 154  
 gcacgtttct cagcatcacc gac 23

<210> 155  
 <211> 50  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 155  
 cgcctgcccct gcaccttcaa ctctgctac acagtgaacc acaaacagtt 50

<210> 156  
 <211> 2680  
 <212> DNA  
 <213> Homo sapiens

<400> 156  
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 gggctgctcc cggatggcct cctgttctct ttgctgctgc taatgctgct 100  
 cgcggaccca gcgctcccgg ccggacgtca cccccagtg gtgctgggtcc 150  
 ctggtgattt gggtaaccaa ctggaagcca agctggacaa gccgacagtg 200  
 gtgcactacc tctgctccaa gaagaccgaa agctacttca caatctggct 250  
 gaacctggaa ctgctgctgc ctgtcatcat tgactgctgg attgacaata 300  
 tcaggctggg ttacaacaaa acatccaggg ccaccagtt tcctgatggg 350  
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 ggaccccagc aaaagcagcg tgggttcta tttccacacc atgggtggaga 450  
 gccttggtggg ctggggctac acacgggggtg aggatgtccg agggggtccc 500



cccccagtcc cgcaggctgt gttccagggg ccctgatttc ctoggatgtg 2000  
 ctattggccc caggactgaa gctgcctccc ttcaccctgg gactgtgggt 2050  
 ccaaggatga gagcaggggt tggagccatg gccttctggg aacctatgga 2100  
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 atgctgtaaa aaaaaaaaaa aaaaaaaaaa 2680

<210> 157

<211> 412

<212> PRT

<213> Artificial

<400> 157

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			20						25					30
Ala	Leu	Pro	Ala	Gly	Arg	His	Pro	Pro	Val	Val	Leu	Val	Pro	Gly
			35						40					45
Asp	Leu	Gly	Asn	Gln	Leu	Glu	Ala	Lys	Leu	Asp	Lys	Pro	Thr	Val
			50						55					60
Val	His	Tyr	Leu	Cys	Ser	Lys	Lys	Thr	Glu	Ser	Tyr	Phe	Thr	Ile
			65						70					75
Trp	Leu	Asn	Leu	Glu	Leu	Leu	Leu	Pro	Val	Ile	Ile	Asp	Cys	Trp
			80						85					90
Ile	Asp	Asn	Ile	Arg	Leu	Val	Tyr	Asn	Lys	Thr	Ser	Arg	Ala	Thr
			95						100					105
Gln	Phe	Pro	Asp	Gly	Val	Asp	Val	Arg	Val	Pro	Gly	Phe	Gly	Lys

				110					115					120
Thr	Phe	Ser	Leu	Glu 125	Phe	Leu	Asp	Pro	Ser 130	Lys	Ser	Ser	Val	Gly 135
Ser	Tyr	Phe	His	Thr 140	Met	Val	Glu	Ser	Leu 145	Val	Gly	Trp	Gly	Tyr 150
Thr	Arg	Gly	Glu	Asp 155	Val	Arg	Gly	Ala	Pro 160	Tyr	Asp	Trp	Arg	Arg 165
Ala	Pro	Asn	Glu	Asn 170	Gly	Pro	Tyr	Phe	Leu 175	Ala	Leu	Arg	Glu	Met 180
Ile	Glu	Glu	Met	Tyr 185	Gln	Leu	Tyr	Gly	Gly 190	Pro	Val	Val	Leu	Val 195
Ala	His	Ser	Met	Gly 200	Asn	Met	Tyr	Thr	Leu 205	Tyr	Phe	Leu	Gln	Arg 210
Gln	Pro	Gln	Ala	Trp 215	Lys	Asp	Lys	Tyr	Ile 220	Arg	Ala	Phe	Val	Ser 225
Leu	Gly	Ala	Pro	Trp 230	Gly	Gly	Val	Ala	Lys 235	Thr	Leu	Arg	Val	Leu 240
Ala	Ser	Gly	Asp	Asn 245	Asn	Arg	Ile	Pro	Val 250	Ile	Gly	Pro	Leu	Lys 255
Ile	Arg	Glu	Gln	Gln 260	Arg	Ser	Ala	Val	Ser 265	Thr	Ser	Trp	Leu	Leu 270
Pro	Tyr	Asn	Tyr	Thr 275	Trp	Ser	Pro	Glu	Lys 280	Val	Phe	Val	Gln	Thr 285
Pro	Thr	Ile	Asn	Tyr 290	Thr	Leu	Arg	Asp	Tyr 295	Arg	Lys	Phe	Phe	Gln 300
Asp	Ile	Gly	Phe	Glu 305	Asp	Gly	Trp	Leu	Met 310	Arg	Gln	Asp	Thr	Glu 315
Gly	Leu	Val	Glu	Ala 320	Thr	Met	Pro	Pro	Gly 325	Val	Gln	Leu	His	Cys 330
Leu	Tyr	Gly	Thr	Gly 335	Val	Pro	Thr	Pro	Asp 340	Ser	Phe	Tyr	Tyr	Glu 345
Ser	Phe	Pro	Asp	Arg 350	Asp	Pro	Lys	Ile	Cys 355	Phe	Gly	Asp	Gly	Asp 360
Gly	Thr	Val	Asn	Leu 365	Lys	Ser	Ala	Leu	Gln 370	Cys	Gln	Ala	Trp	Gln 375
Ser	Arg	Gln	Glu	His 380	Gln	Val	Leu	Leu	Gln 385	Glu	Leu	Pro	Gly	Ser 390
Glu	His	Ile	Glu	Met 395	Leu	Ala	Asn	Ala	Thr 400	Thr	Leu	Ala	Tyr	Leu 405

Lys Arg Val Leu Gly Pro  
410

<210> 158

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 158

ctggggctac acacggggtg agg 23

<210> 159

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 159

ggtgccgctg cagaaagtag agcg 24

<210> 160

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 160

gccccaaatg aaaacggggc ctacttcctg gccctccgag agatg 45

<210> 161

<211> 1512

<212> DNA

<213> Homo sapiens

<400> 161

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atggagagcg gggcctacgg cgcggccaag gcgggcgagg ccttcgacct 100

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10017001-100401



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Glu	Gly	Tyr	Ser	Asn	Ala	His	Glu	Ser	Lys	Gln	Met	Tyr	Cys	Val	
				50					55					60	
Phe	Asn	Arg	Asn	Glu	Asp	Ala	Cys	Arg	Tyr	Gly	Ser	Ala	Ile	Gly	
				65					70					75	
Val	Leu	Ala	Phe	Leu	Ala	Ser	Ala	Phe	Phe	Leu	Val	Val	Asp	Ala	
				80					85					90	
Tyr	Phe	Pro	Gln	Ile	Ser	Asn	Ala	Thr	Asp	Arg	Lys	Tyr	Leu	Val	
				95					100					105	
Ile	Gly	Asp	Leu	Leu	Phe	Ser	Ala	Leu	Trp	Thr	Phe	Leu	Trp	Phe	
				110					115					120	
Val	Gly	Phe	Cys	Phe	Leu	Thr	Asn	Gln	Trp	Ala	Val	Thr	Asn	Pro	
				125					130					135	
Lys	Asp	Val	Leu	Val	Gly	Ala	Asp	Ser	Val	Arg	Ala	Ala	Ile	Thr	
				140					145					150	
Phe	Ser	Phe	Phe	Ser	Ile	Phe	Ser	Trp	Gly	Val	Leu	Ala	Ser	Leu	
				155					160					165	
Ala	Tyr	Gln	Arg	Tyr	Lys	Ala	Gly	Val	Asp	Asp	Phe	Ile	Gln	Asn	
				170					175					180	
Tyr	Val	Asp	Pro	Thr	Pro	Asp	Pro	Asn	Thr	Ala	Tyr	Ala	Ser	Tyr	
				185					190					195	
Pro	Gly	Ala	Ser	Val	Asp	Asn	Tyr	Gln	Gln	Pro	Pro	Phe	Thr	Gln	
				200					205					210	
Asn	Ala	Glu	Thr	Thr	Glu	Gly	Tyr	Gln	Pro	Pro	Pro	Val	Tyr		
				215					220						

<210> 163

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 163

tggtcttcgc cttgatcgtg ttct 24

<210> 164

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe





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 ctggttcatt ctccaaatcc ccgagcacog ccggctgatg ctgagccccg 550  
 aggtggtgca ggcactgctg gtggaggagc tgctgtccac agtcaacagc 600  
 tcggctgccg tcccctacag ggccgagtag gaagtggacc ccgagggcct 650  
 agtgatcctg gaagccagtg tgaaagacat agctgcattg aattccacgc 700  
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<210> 169  
 <211> 802  
 <212> PRT  
 <213> Homo sapiens  
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Cys	Glu	Asp	Ser	Lys	Arg	Lys	Ala	Arg	Gly	Tyr	Leu	Arg	Leu	Val	35	40	45	
Pro	Leu	Phe	Val	Leu	Leu	Ala	Leu	Leu	Val	Leu	Ala	Ser	Ala	Gly	50	55	60	
Val	Leu	Leu	Trp	Tyr	Phe	Leu	Gly	Tyr	Lys	Ala	Glu	Val	Met	Val	65	70	75	
Ser	Gln	Val	Tyr	Ser	Gly	Ser	Leu	Arg	Val	Leu	Asn	Arg	His	Phe	80	85	90	
Ser	Gln	Asp	Leu	Thr	Arg	Arg	Glu	Ser	Ser	Ala	Phe	Arg	Ser	Glu	95	100	105	
Thr	Ala	Lys	Ala	Gln	Lys	Met	Leu	Lys	Glu	Leu	Ile	Thr	Ser	Thr	110	115	120	
Arg	Leu	Gly	Thr	Tyr	Tyr	Asn	Ser	Ser	Ser	Val	Tyr	Ser	Phe	Gly	125	130	135	
Glu	Gly	Pro	Leu	Thr	Cys	Phe	Phe	Trp	Phe	Ile	Leu	Gln	Ile	Pro	140	145	150	
Glu	His	Arg	Arg	Leu	Met	Leu	Ser	Pro	Glu	Val	Val	Gln	Ala	Leu	155	160	165	
Leu	Val	Glu	Glu	Leu	Leu	Ser	Thr	Val	Asn	Ser	Ser	Ala	Ala	Val	170	175	180	
Pro	Tyr	Arg	Ala	Glu	Tyr	Glu	Val	Asp	Pro	Glu	Gly	Leu	Val	Ile	185	190	195	
Leu	Glu	Ala	Ser	Val	Lys	Asp	Ile	Ala	Ala	Leu	Asn	Ser	Thr	Leu	200	205	210	
Gly	Cys	Tyr	Arg	Tyr	Ser	Tyr	Val	Gly	Gln	Gly	Gln	Val	Leu	Arg	215	220	225	
Leu	Lys	Gly	Pro	Asp	His	Leu	Ala	Ser	Ser	Cys	Leu	Trp	His	Leu	230	235	240	
Gln	Gly	Pro	Lys	Asp	Leu	Met	Leu	Lys	Leu	Arg	Leu	Glu	Trp	Thr	245	250	255	
Leu	Ala	Glu	Cys	Arg	Asp	Arg	Leu	Ala	Met	Tyr	Asp	Val	Ala	Gly	260	265	270	
Pro	Leu	Glu	Lys	Arg	Leu	Ile	Thr	Ser	Val	Tyr	Gly	Cys	Ser	Arg	275	280	285	
Gln	Glu	Pro	Val	Val	Glu	Val	Leu	Ala	Ser	Gly	Ala	Ile	Met	Ala				

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Lys Gly Leu His Ser	305	Tyr Tyr Asp Pro Phe	310	Val	315
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Thr Leu Asp Asn	335	Gly Val Leu Ser Thr	340	Pro	345
Tyr Phe Pro Ser	350	Thr His Cys Ser Trp	355	His	360
Leu Thr Val Pro	365	Leu Ala Leu Trp Phe	370	Asp	375
Ala Tyr Ala Leu	380	Asp Leu Pro Cys Thr	385	Gln	390
Gly Gln Trp Thr	395	Leu Cys Gly Leu Arg	400	Ile	405
Leu Gln Pro Tyr	410	Val Val Ala Thr Ala	415	Gly	420
Ile Thr Ile Asn	425	Ser Leu Thr Gly Pro	430	Gly	435
Val Arg Val His	440	Gln Ser Asp Pro Cys	445	Pro	450
Gly Glu Phe Leu	455	Leu Cys Val Pro Ala	460	Cys	465
Asp Gly Val Lys	470	Leu Asp Glu Arg Asn	475	Cys	480
Val Cys Arg Ala	485	Glu Asp Ser Thr Cys	490	Ile	495
Ser Leu Pro Lys	500	Pro Asp Cys Leu Asn	505	Gly	510
Ser Asp Glu Glu	515	Val Pro Cys Gly Thr	520	Phe	525
Thr Phe Gln Cys	530	Val Lys Lys Pro Asn	535	Pro	540
Gln Cys Asp Gly	545	Asp Gly Ser Asp Glu	550	Glu	555
His Cys Asp Cys	560	Ser Ser Arg Ile Val	565	Gly	570
Gly Ala Val Ser	575	Pro Trp Gln Ala Ser	580	Leu	585

Gln	Val	Arg	Gly	Arg 590	His	Ile	Cys	Gly	Gly 595	Ala	Leu	Ile	Ala	Asp 600
Arg	Trp	Val	Ile	Thr 605	Ala	Ala	His	Cys	Phe 610	Gln	Glu	Asp	Ser	Met 615
Ala	Ser	Thr	Val	Leu 620	Trp	Thr	Val	Phe	Leu 625	Gly	Lys	Val	Trp	Gln 630
Asn	Ser	Arg	Trp	Pro 635	Gly	Glu	Val	Ser	Phe 640	Lys	Val	Ser	Arg	Leu 645
Leu	Leu	His	Pro	Tyr 650	His	Glu	Glu	Asp	Ser 655	His	Asp	Tyr	Asp	Val 660
Ala	Leu	Leu	Gln	Leu 665	Asp	His	Pro	Val	Val 670	Arg	Ser	Ala	Ala	Val 675
Arg	Pro	Val	Cys	Leu 680	Pro	Ala	Arg	Ser	His 685	Phe	Phe	Glu	Pro	Gly 690
Leu	His	Cys	Trp	Ile 695	Thr	Gly	Trp	Gly	Ala 700	Leu	Arg	Glu	Gly	Gly 705
Pro	Ile	Ser	Asn	Ala 710	Leu	Gln	Lys	Val	Asp 715	Val	Gln	Leu	Ile	Pro 720
Gln	Asp	Leu	Cys	Ser 725	Glu	Ala	Tyr	Arg	Tyr 730	Gln	Val	Thr	Pro	Arg 735
Met	Leu	Cys	Ala	Gly 740	Tyr	Arg	Lys	Gly	Lys 745	Lys	Asp	Ala	Cys	Gln 750
Gly	Asp	Ser	Gly	Gly 755	Pro	Leu	Val	Cys	Lys 760	Ala	Leu	Ser	Gly	Arg 765
Trp	Phe	Leu	Ala	Gly 770	Leu	Val	Ser	Trp	Gly 775	Leu	Gly	Cys	Gly	Arg 780
Pro	Asn	Tyr	Phe	Gly 785	Val	Tyr	Thr	Arg	Ile 790	Thr	Gly	Val	Ile	Ser 795
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<211> 1327
<212> DNA
<213> Homo sapiens
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tgcaactatgg cttgtacaac cagtcggacc cctgccctgg aqaattcctc 200
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 gcaaagagga cagcacatgc atctcactgc ccaaggtctg tgatgggcag 350  
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<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 171

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<210> 172

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 <210> 174  
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 <223> Synthetic oligonucleotide probe  
  
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 <213> Artificial Sequence  
  
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 <210> 177  
 <211> 1510  
 <212> DNA  
 <213> Homo sapiens



<400> 177

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aaaaaaaaaa 1510

<210> 178

<211> 354

<212> PRT

<213> Homo sapiens

<400> 178

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Cys Phe Ala Ala Gly Ser Pro Val Pro Phe Gly Pro Glu Gly Arg  
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35 40 45

Lys Pro Ser Val Arg Phe Asn Leu Arg Thr Ser Lys Asp Pro Glu  
50 55 60

His Glu Gly Cys Tyr Leu Ser Val Gly His Ser Gln Pro Leu Glu  
65 70 75

Asp Cys Ser Phe Asn Met Thr Ala Lys Thr Phe Phe Ile Ile His  
80 85 90

Gly Trp Thr Met Ser Gly Ile Phe Glu Asn Trp Leu His Lys Leu  
95 100 105

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Val Ser Ala Leu His Thr Arg Glu Lys Asp Ala Asn Val Val Val
                110                115                120
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Val	Asp	Trp	Leu	Pro	Leu	Ala	His	Gln	Leu	Tyr	Thr	Asp	Ala	Val
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Asn Asn Thr Arg Val Val Gly His Ser Ile Ala Arg Met Leu Asp  
140 145 150

Trp Leu Gln Glu Lys Asp Asp Phe Ser Leu Gly Asn Val His Leu  
155 160 165

Ile Gly Tyr Ser Leu Gly Ala His Val Ala Gly Tyr Ala Gly Asn  
170 175 180

Phe Val Lys Gly Thr Val Gly Arg Ile Thr Gly Leu Asp Pro Ala  
185 190 195

Gly Pro Met Phe Glu Gly Ala Asp Ile His Lys Arg Leu Ser Pro  
200 205 210

Asp Asp Ala Asp Phe Val Asp Val Leu His Thr Tyr Thr Arg Ser  
215 220 225

Phe Gly Leu Ser Ile Gly Ile Gln Met Pro Val Gly His Ile Asp  
230 235 240

Ile	Tyr	Pro	Asn	Gly	Gly	Asp	Phe	Gln	Pro	Gly	Cys	Gly	Leu	Asn
				245					250					255
Asp	Val	Leu	Gly	Ser	Ile	Ala	Tyr	Gly	Thr	Ile	Thr	Glu	Val	Val
				260					265					270
Lys	Cys	Glu	His	Glu	Arg	Ala	Val	His	Leu	Phe	Val	Asp	Ser	Leu
				275					280					285
Val	Asn	Gln	Asp	Lys	Pro	Ser	Phe	Ala	Phe	Gln	Cys	Thr	Asp	Ser
				290					295					300
Asn	Arg	Phe	Lys	Lys	Gly	Ile	Cys	Leu	Ser	Cys	Arg	Lys	Asn	Arg
				305					310					315
Cys	Asn	Ser	Ile	Gly	Tyr	Asn	Ala	Lys	Lys	Met	Arg	Asn	Lys	Arg
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Asn	Ser	Lys	Met	Tyr	Leu	Lys	Thr	Arg	Ala	Gly	Met	Pro	Phe	Arg
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Gly	Asn	Leu	Gln	Ser	Leu	Glu	Cys	Pro						
				350										

<210> 179

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 179

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<210> 180

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 180

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<210> 181

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<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 181

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<210> 182

<211> 3240  
<212> DNA  
<213> Homo sapiens

<400> 182

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acgcgctgga ggagtggagc agcaccggc cgccctggg ggctgacagt 150  
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 tgggcagaac ctgaggtttt gccatccaca atccctccta cagggcctgg 3150  
 ctcacaaaaa gagtgcaca aatgcttcta ttccatagct acggcattgc 3200  
 tcagtaagtt gaggtcaaaa ataaaggaat catacatctc 3240

<210> 183  
 <211> 713  
 <212> PRT  
 <213> Homo sapiens

<400> 183  
 Met Leu Leu Ala Thr Leu Leu Leu Leu Leu Leu Gly Gly Ala Leu  
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                     20                    25                    30  
 Pro Pro Ala Val Leu Leu Glu Val Gln Gly Thr Leu Gln Arg Pro  
                     35                    40                    45  
 Leu Val Arg Asp Ser Arg Thr Ser Pro Ala Asn Cys Thr Trp Leu  
                     50                    55                    60  
 Ile Leu Gly Ser Lys Glu Gln Thr Val Thr Ile Arg Phe Gln Lys  
                     65                    70                    75  
 Leu His Leu Ala Cys Gly Ser Glu Arg Leu Thr Leu Arg Ser Pro  
                     80                    85                    90  
 Leu Gln Pro Leu Ile Ser Leu Cys Glu Ala Pro Pro Ser Pro Leu  
                     95                    100                    105  
 Gln Leu Pro Gly Gly Asn Val Thr Ile Thr Tyr Ser Tyr Ala Gly  
                     110                    115                    120  
 Ala Arg Ala Pro Met Gly Gln Gly Phe Leu Leu Ser Tyr Ser Gln  
                     125                    130                    135  
 Asp Trp Leu Met Cys Leu Gln Glu Glu Phe Gln Cys Leu Asn His  
                     140                    145                    150  
 Arg Cys Val Ser Ala Val Gln Arg Cys Asp Gly Val Asp Ala Cys  
                     155                    160                    165  
 Gly Asp Gly Ser Asp Glu Ala Gly Cys Ser Ser Asp Pro Phe Pro

	170		175		180
Gly Leu Thr Pro	Arg 185	Pro Val Pro Ser	Leu 190	Pro Cys Asn Val	Thr 195
Leu Glu Asp Phe	Tyr 200	Gly Val Phe Ser	Ser 205	Pro Gly Tyr Thr	His 210
Leu Ala Ser Val	Ser 215	His Pro Gln Ser	Cys 220	His Trp Leu Leu	Asp 225
Pro His Asp Gly	Arg 230	Arg Leu Ala Val	Arg 235	Phe Thr Ala Leu	Asp 240
Leu Gly Phe Gly	Asp 245	Ala Val His Val	Tyr 250	Asp Gly Pro Gly	Pro 255
Pro Glu Ser Ser	Arg 260	Leu Leu Arg Ser	Leu 265	Thr His Phe Ser	Asn 270
Gly Lys Ala Val	Thr 275	Val Glu Thr Leu	Ser 280	Gly Gln Ala Val	Val 285
Ser Tyr His Thr	Val 290	Ala Trp Ser Asn	Gly 295	Arg Gly Phe Asn	Ala 300
Thr Tyr His Val	Arg 305	Gly Tyr Cys Leu	Pro 310	Trp Asp Arg Pro	Cys 315
Gly Leu Gly Ser	Gly 320	Leu Gly Ala Gly	Glu 325	Gly Leu Gly Glu	Arg 330
Cys Tyr Ser Glu	Ala 335	Gln Arg Cys Asp	Gly 340	Ser Trp Asp Cys	Ala 345
Asp Gly Thr Asp	Glu 350	Glu Asp Cys Pro	Gly 355	Cys Pro Pro Gly	His 360
Phe Pro Cys Gly	Ala 365	Ala Gly Thr Ser	Gly 370	Ala Thr Ala Cys	Tyr 375
Leu Pro Ala Asp	Arg 380	Cys Asn Tyr Gln	Thr 385	Phe Cys Ala Asp	Gly 390
Ala Asp Glu Arg	Arg 395	Cys Arg His Cys	Gln 400	Pro Gly Asn Phe	Arg 405
Cys Arg Asp Glu	Lys 410	Cys Val Tyr Glu	Thr 415	Trp Val Cys Asp	Gly 420
Gln Pro Asp Cys	Ala 425	Asp Gly Ser Asp	Glu 430	Trp Asp Cys Ser	Tyr 435
Val Leu Pro Arg	Lys 440	Val Ile Thr Ala	Ala 445	Val Ile Gly Ser	Leu 450
Val Cys Gly Leu	Leu 455	Leu Val Ile Ala	Leu 460	Gly Cys Thr Cys	Lys 465

Leu Tyr Ala Ile	Arg Thr Gln Glu Tyr	Ser Ile Phe Ala Pro	Leu
	470	475	480
Ser Arg Met Glu	Ala Glu Ile Val Gln	Gln Gln Ala Pro Pro	Ser
	485	490	495
Tyr Gly Gln Leu	Ile Ala Gln Gly Ala	Ile Pro Pro Val Glu	Asp
	500	505	510
Phe Pro Thr Glu	Asn Pro Asn Asp Asn	Ser Val Leu Gly Asn	Leu
	515	520	525
Arg Ser Leu Leu	Gln Ile Leu Arg Gln	Asp Met Thr Pro Gly	Gly
	530	535	540
Gly Pro Gly Ala	Arg Arg Arg Gln Arg	Gly Arg Leu Met Arg	Arg
	545	550	555
Leu Val Arg Arg	Leu Arg Arg Trp Gly	Leu Leu Pro Arg Thr	Asn
	560	565	570
Thr Pro Ala Arg	Ala Ser Glu Ala Arg	Ser Gln Val Thr Pro	Ser
	575	580	585
Ala Ala Pro Leu	Glu Ala Leu Asp Gly	Gly Thr Gly Pro Ala	Arg
	590	595	600
Glu Gly Gly Ala	Val Gly Gly Gln Asp	Gly Glu Gln Ala Pro	Pro
	605	610	615
Leu Pro Ile Lys	Ala Pro Leu Pro Ser	Ala Ser Thr Ser Pro	Ala
	620	625	630
Pro Thr Thr Val	Pro Glu Ala Pro Gly	Pro Leu Pro Ser Leu	Pro
	635	640	645
Leu Glu Pro Ser	Leu Leu Ser Gly Val	Val Gln Ala Leu Arg	Gly
	650	655	660
Arg Leu Leu Pro	Ser Leu Gly Pro Pro	Gly Pro Thr Arg Ser	Pro
	665	670	675
Pro Gly Pro His	Thr Ala Val Leu Ala	Leu Glu Asp Glu Asp	Asp
	680	685	690
Val Leu Leu Val	Pro Leu Ala Glu Pro	Gly Val Trp Val Ala	Glu
	695	700	705
Ala Glu Asp Glu	Pro Leu Leu Thr		
	710		

<210> 184

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe



<400> 184  
ggctgtcact gtggagacac 20

<210> 185  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 185  
gcaaggtcat tacagctg 18

<210> 186  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 186  
agaacatagg agcagtccca ctc 23

<210> 187  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 187  
tgcctgctgc tgcacaatct cag 23

<210> 188  
<211> 45  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 188  
ggctattgct tgccttgga cagaccctgt ggcttaggct ctggc 45

<210> 189  
<211> 663  
<212> DNA  
<213> Homo sapiens

<400> 189  
cgagctgggc gagaagtagg ggagggcggt gctccgccgc ggtggcggtt 50  
gctatcgctt cgcagaacct actcaggcag ccagctgaga agagttgagg 100  
gaaagtgctg ctgctgggtc tgcagacgcg atggataacg tgcagccgaa 150



Val Leu

<210> 191  
<211> 495  
<212> DNA  
<213> Homo sapiens

<220>  
<221> unsure  
<222> 78, 212, 234, 487  
<223> unknown base

<400> 191  
gggcgagaag taggggaggg cgtgttccgc cgcggtggcg gttgctatcg 50  
ttttgcagaa cctactcagg cagccagntg agaagagttg agggaaagtg 100  
ctgctgctgg gtctgcagac gcgatggata acgtgcagcc gaaaataaaa 150  
catcgcccct tctgcttcag tgtgaaaggc cacgtgaaga tgctgcggct 200  
ggcactaact gngacatcta tgaccttttt tatnatcgca caagcccctg 250  
aaccatatat tgttatcact ggatttgaag tcaccgttat cttatttttc 300  
atacttttat atgtactcag acttgatcga ttaatgaagt ggttattttg 350  
gcctttgctt gatattatca actcactggg aacaacagta ttcatgctca 400  
tcgtatctgt gttggcactg ataccagaaa ccacaacatt gacagttggt 450  
ggaggggtgt ttgcacttgt gacagcagta tgctgtnttg ccgac 495

<210> 192  
<211> 25  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 192  
cgttttgcag aacctactca ggcag 25

<210> 193  
<211> 25  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 193  
cctccaccaa ctgtcaatgt tgtgg 25

<210> 194  
<211> 40

<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 194  
aaagtgtctg tgctgggtct gcagacgcga tggataacgt 40

<210> 195  
<211> 1879  
<212> DNA  
<213> Homo sapien

<400> 195  
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cactggcccc ggcgctgctg ctgcctctgc tggcccagtg gctcctgcgc 150  
gccgccccgg agctggcccc cgcgcccttc acgctgcccc tccgggtggc 200  
cgcgggccacg aaccgcgtag ttgcgcccac cccgggaacc gggaccctg 250  
ccgagcgcca cgccgacggc ttggcgctcg ccttgagacc tgccctggcg 300  
tcccccgcg ggcgcgcca cttcttggcc atggtagaca acctgcaggg 350  
ggactctggc cgcggtact acctggagat gctgatcggg accccccgc 400  
agaagctaca gattctcggt gacactggaa gcagtaactt tgccgtggca 450  
ggaacccgc actcctacat agacacgtac tttgacacag agaggtctag 500  
cacataccgc tccaagggct ttgacgtcac agtgaagtac acacaaggaa 550  
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aatacttctt ttcttgtcaa cattgccact atttttgaat cagagaattt 650  
ctttttgcct gggattaaat ggaatggaat acttggccta gcttatgcc 700  
cacttgccaa gccatcaagt tctctggaga ccttcttoga ctccctggtg 750  
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gaagagtggg actaccagat agaaattctg aaattggaaa ttggaggcca 950  
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acagtggcac cacgctgctg cgcctgcccc agaaggtgtt tgatgcggtg 1050  
gtggaagctg tggcccgcg atctctgatt ccagaattct ctgatggttt 1100



Gln	Ile	Leu	Val	Asp	Thr	Gly	Ser	Ser	Asn	Phe	Ala	Val	Ala	Gly	
				110					115					120	
Thr	Pro	His	Ser	Tyr	Ile	Asp	Thr	Tyr	Phe	Asp	Thr	Glu	Arg	Ser	
				125					130					135	
Ser	Thr	Tyr	Arg	Ser	Lys	Gly	Phe	Asp	Val	Thr	Val	Lys	Tyr	Thr	
				140					145					150	
Gln	Gly	Ser	Trp	Thr	Gly	Phe	Val	Gly	Glu	Asp	Leu	Val	Thr	Ile	
				155					160					165	
Pro	Lys	Gly	Phe	Asn	Thr	Ser	Phe	Leu	Val	Asn	Ile	Ala	Thr	Ile	
				170					175					180	
Phe	Glu	Ser	Glu	Asn	Phe	Phe	Leu	Pro	Gly	Ile	Lys	Trp	Asn	Gly	
				185					190					195	
Ile	Leu	Gly	Leu	Ala	Tyr	Ala	Thr	Leu	Ala	Lys	Pro	Ser	Ser	Ser	
				200					205					210	
Leu	Glu	Thr	Phe	Phe	Asp	Ser	Leu	Val	Thr	Gln	Ala	Asn	Ile	Pro	
				215					220					225	
Asn	Val	Phe	Ser	Met	Gln	Met	Cys	Gly	Ala	Gly	Leu	Pro	Val	Ala	
				230					235					240	
Gly	Ser	Gly	Thr	Asn	Gly	Gly	Ser	Leu	Val	Leu	Gly	Gly	Ile	Glu	
				245					250					255	
Pro	Ser	Leu	Tyr	Lys	Gly	Asp	Ile	Trp	Tyr	Thr	Pro	Ile	Lys	Glu	
				260					265					270	
Glu	Trp	Tyr	Tyr	Gln	Ile	Glu	Ile	Leu	Lys	Leu	Glu	Ile	Gly	Gly	
				275					280					285	
Gln	Ser	Leu	Asn	Leu	Asp	Cys	Arg	Glu	Tyr	Asn	Ala	Asp	Lys	Ala	
				290					295					300	
Ile	Val	Asp	Ser	Gly	Thr	Thr	Leu	Leu	Arg	Leu	Pro	Gln	Lys	Val	
				305					310					315	
Phe	Asp	Ala	Val	Val	Glu	Ala	Val	Ala	Arg	Ala	Ser	Leu	Ile	Pro	
				320					325					330	
Glu	Phe	Ser	Asp	Gly	Phe	Trp	Thr	Gly	Ser	Gln	Leu	Ala	Cys	Trp	
				335					340					345	
Thr	Asn	Ser	Glu	Thr	Pro	Trp	Ser	Tyr	Phe	Pro	Lys	Ile	Ser	Ile	
				350					355					360	
Tyr	Leu	Arg	Asp	Glu	Asn	Ser	Ser	Arg	Ser	Phe	Arg	Ile	Thr	Ile	
				365					370					375	
Leu	Pro	Gln	Leu	Tyr	Ile	Gln	Pro	Met	Met	Gly	Ala	Gly	Leu	Asn	
				380					385					390	
Tyr	Glu	Cys	Tyr	Arg	Phe	Gly	Ile	Ser	Pro	Ser	Thr	Asn	Ala	Leu	



<210> 200  
 <211> 19  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 200  
 gccttggtc gttctcttc 19

<210> 201  
 <211> 18  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 201  
 ggtcctgtgc ctggatgg 18

<210> 202  
 <211> 22  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 202  
 gacaagacta cctccgttg tc 22

<210> 203  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 203  
 tgatgcacag ttcagcacct gttg 24

<210> 204  
 <211> 47  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 204  
 cgctccaagg gctttgacgt cacagtgaag tacacacaag gaagctg 47

<210> 205  
 <211> 1939  
 <212> DNA



<213> Homo sapiens

<400> 205

cgcctccgcc ttcggaggct gacgcgcccg ggcgcogttc caggcctgtg 50  
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 ttccgggcgg atgcagggct ggggtcatct gtatctgaag cccctcggaa 1900  
 taaagcgcgt tgaccgccaa aaaaaaaaaa aaaaaaaaaa 1939

<210> 206  
 <211> 377  
 <212> PRT  
 <213> Homo sapiens

<400> 206  
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                     20                    25                    30  
 Met Gly Asn Leu Arg Gly Arg Thr Ala Val Val Thr Gly Ala Asn  
                     35                    40                    45  
 Ser Gly Ile Gly Lys Met Thr Ala Leu Glu Leu Ala Arg Arg Gly  
                     50                    55                    60  
 Ala Arg Val Val Leu Ala Cys Arg Ser Gln Glu Arg Gly Glu Ala  
                     65                    70                    75  
 Ala Ala Phe Asp Leu Arg Gln Glu Ser Gly Asn Asn Glu Val Ile  
                     80                    85                    90  
 Phe Met Ala Leu Asp Leu Ala Ser Leu Ala Ser Val Arg Ala Phe  
                     95                    100                    105  
 Ala Thr Ala Phe Leu Ser Ser Glu Pro Arg Leu Asp Ile Leu Ile  
                     110                    115                    120  
 His Asn Ala Gly Ile Ser Ser Cys Gly Arg Thr Arg Glu Ala Phe  
                     125                    130                    135  
 Asn Leu Leu Leu Arg Val Asn His Ile Gly Pro Phe Leu Leu Thr  
                     140                    145                    150



<210> 208  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 208  
 acgccagtgg cctcaagctg gttg 24

<210> 209  
 <211> 45  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 209  
 ctttctgagc tctgagccac ggttggacat cctcatccac aatgc 45

<210> 210  
 <211> 3716  
 <212> DNA  
 <213> Homo sapiens

<400> 210  
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 gctcatcatg ggaggcatgg ctgaggactc cccgccccag atcctagtcc 100  
 acccccagga ccagctgttc cagggccctg gccctgccag gatgagctgc 150  
 caagcctcag gccagccacc tcccaccatc cgctgggttg tgaatgggca 200  
 gccctgagc atggtgcccc cagaccacaca ccacctcctg cctgatggga 250  
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 gccctgtcca cagacctggg tgtctacaca tgtgaggcca gcaaccggct 350  
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<211> 985

<212> PRT

<213> Homo sapiens

<400> 211

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Cys	Gln	Ala	Ser	Gly	Gln	Pro	Pro	Pro	Thr	Ile	Arg	Trp	Leu	Leu
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Asn	Gly	Gln	Pro	Leu	Ser	Met	Val	Pro	Pro	Asp	Pro	His	His	Leu
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Leu	Pro	Asp	Gly	Thr	Leu	Leu	Leu	Leu	Gln	Pro	Pro	Ala	Arg	Gly
				65					70					75
His	Ala	His	Asp	Gly	Gln	Ala	Leu	Ser	Thr	Asp	Leu	Gly	Val	Tyr
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Thr	Cys	Glu	Ala	Ser	Asn	Arg	Leu	Gly	Thr	Ala	Val	Ser	Arg	Gly
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Ala	Arg	Leu	Ser	Val	Ala	Val	Leu	Arg	Glu	Asp	Phe	Gln	Ile	Gln
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Pro	Arg	Asp	Met	Val	Ala	Val	Val	Gly	Glu	Gln	Phe	Thr	Leu	Glu
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Cys	Gly	Pro	Pro	Trp	Gly	His	Pro	Glu	Pro	Thr	Val	Ser	Trp	Trp
				140					145					150
Lys	Asp	Gly	Lys	Pro	Leu	Ala	Leu	Gln	Pro	Gly	Arg	His	Thr	Val
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Ser	Gly	Gly	Ser	Leu	Leu	Met	Ala	Arg	Ala	Glu	Lys	Ser	Asp	Glu
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Gly	Thr	Tyr	Met	Cys	Val	Ala	Thr	Asn	Ser	Ala	Gly	His	Arg	Glu
				185					190					195
Ser	Arg	Ala	Ala	Arg	Val	Ser	Ile	Gln	Glu	Pro	Gln	Asp	Tyr	Thr
				200					205					210
Glu	Pro	Val	Glu	Leu	Leu	Ala	Val	Arg	Ile	Gln	Leu	Glu	Asn	Val
				215					220					225
Thr	Leu	Leu	Asn	Pro	Asp	Pro	Ala	Glu	Gly	Pro	Lys	Pro	Arg	Pro
				230					235					240

Ala Val Trp Leu	Ser Trp Lys Val Ser	Gly Pro Ala Ala Pro	Ala
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Gln Ser Tyr Thr	Ala Leu Phe Arg Thr	Gln Thr Ala Pro Gly	Gly
260	265	270	
Gln Gly Ala Pro	Trp Ala Glu Glu Leu	Leu Ala Gly Trp Gln	Ser
275	280	285	
Ala Glu Leu Gly	Gly Leu His Trp Gly	Gln Asp Tyr Glu Phe	Lys
290	295	300	
Val Arg Pro Ser	Ser Gly Arg Ala Arg	Gly Pro Asp Ser Asn	Val
305	310	315	
Leu Leu Leu Arg	Leu Pro Glu Lys Val	Pro Ser Ala Pro Pro	Gln
320	325	330	
Glu Val Thr Leu	Lys Pro Gly Asn Gly	Thr Val Phe Val Ser	Trp
335	340	345	
Val Pro Pro Pro	Ala Glu Asn His Asn	Gly Ile Ile Arg Gly	Tyr
350	355	360	
Gln Val Trp Ser	Leu Gly Asn Thr Ser	Leu Pro Pro Ala Asn	Trp
365	370	375	
Thr Val Val Gly	Glu Gln Thr Gln Leu	Glu Ile Ala Thr His	Met
380	385	390	
Pro Gly Ser Tyr	Cys Val Gln Val Ala	Ala Val Thr Gly Ala	Gly
395	400	405	
Ala Gly Glu Pro	Ser Arg Pro Val Cys	Leu Leu Leu Glu Gln	Ala
410	415	420	
Met Glu Arg Ala	Thr Gln Glu Pro Ser	Glu His Gly Pro Trp	Thr
425	430	435	
Leu Glu Gln Leu	Arg Ala Thr Leu Lys	Arg Pro Glu Val Ile	Ala
440	445	450	
Thr Cys Gly Val	Ala Leu Trp Leu Leu	Leu Leu Gly Thr Ala	Val
455	460	465	
Cys Ile His Arg	Arg Arg Arg Ala Arg	Val His Leu Gly Pro	Gly
470	475	480	
Leu Tyr Arg Tyr	Thr Ser Glu Asp Ala	Ile Leu Lys His Arg	Met
485	490	495	
Asp His Ser Asp	Ser Gln Trp Leu Ala	Asp Thr Trp Arg Ser	Thr
500	505	510	
Ser Gly Ser Arg	Asp Leu Ser Ser Ser	Ser Ser Leu Ser Ser	Arg
515	520	525	
Leu Gly Ala Asp	Ala Arg Asp Pro Leu	Asp Cys Arg Arg Ser	Leu



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Leu	Ser	Trp	Asp	Ser 545	Arg	Ser	Pro	Gly	Val 550	Pro	Leu	Leu	Pro	Asp 555				
Thr	Ser	Thr	Phe	Tyr 560	Gly	Ser	Leu	Ile	Ala 565	Glu	Leu	Pro	Ser	Ser 570				
Thr	Pro	Ala	Arg	Pro 575	Ser	Pro	Gln	Val	Pro 580	Ala	Val	Arg	Arg	Leu 585				
Pro	Pro	Gln	Leu	Ala 590	Gln	Leu	Ser	Ser	Pro 595	Cys	Ser	Ser	Ser	Asp 600				
Ser	Leu	Cys	Ser	Arg 605	Arg	Gly	Leu	Ser	Ser 610	Pro	Arg	Leu	Ser	Leu 615				
Ala	Pro	Ala	Glu	Ala 620	Trp	Lys	Ala	Lys	Lys 625	Lys	Gln	Glu	Leu	Gln 630				
His	Ala	Asn	Ser	Ser 635	Pro	Leu	Leu	Arg	Gly 640	Ser	His	Ser	Leu	Glu 645				
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Gln	Ser	Pro	Gly	Ala 665	Val	Pro	Gln	Ala	Leu 670	Val	Ala	Trp	Arg	Ala 675				
Leu	Gly	Pro	Lys	Leu 680	Leu	Ser	Ser	Ser	Asn 685	Glu	Leu	Val	Thr	Arg 690				
His	Leu	Pro	Pro	Ala 695	Pro	Leu	Phe	Pro	His 700	Glu	Thr	Pro	Pro	Thr 705				
Gln	Ser	Gln	Gln	Thr 710	Gln	Pro	Pro	Val	Ala 715	Pro	Gln	Ala	Pro	Ser 720				
Ser	Ile	Leu	Leu	Pro 725	Ala	Ala	Pro	Ile	Pro 730	Ile	Leu	Ser	Pro	Cys 735				
Ser	Pro	Pro	Ser	Pro 740	Gln	Ala	Ser	Ser	Leu 745	Ser	Gly	Pro	Ser	Pro 750				
Ala	Ser	Ser	Arg	Leu 755	Ser	Ser	Ser	Ser	Leu 760	Ser	Ser	Leu	Gly	Glu 765				
Asp	Gln	Asp	Ser	Val 770	Leu	Thr	Pro	Glu	Glu 775	Val	Ala	Leu	Cys	Leu 780				
Glu	Leu	Ser	Glu	Gly 785	Glu	Glu	Thr	Pro	Arg 790	Asn	Ser	Val	Ser	Pro 795				
Met	Pro	Arg	Ala	Pro 800	Ser	Pro	Pro	Thr	Thr 805	Tyr	Gly	Tyr	Ile	Ser 810				
Val	Pro	Thr	Ala	Ser 815	Glu	Phe	Thr	Asp	Met 820	Gly	Arg	Thr	Gly	Gly 825				

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Cys	Leu	Thr	Pro	Thr	Pro	Ser	Glu	Gly	Ser	Leu	Ala	Asn	Gly	Trp	
				845					850					855	
Gly	Ser	Ala	Ser	Glu	Asp	Asn	Ala	Ala	Ser	Ala	Arg	Ala	Ser	Leu	
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Val	Ser	Ser	Ser	Asp	Gly	Ser	Phe	Leu	Ala	Asp	Ala	His	Phe	Ala	
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Arg	Ala	Leu	Ala	Val	Ala	Val	Asp	Ser	Phe	Gly	Phe	Gly	Leu	Glu	
				890					895					900	
Pro	Arg	Glu	Ala	Asp	Cys	Val	Phe	Ile	Asp	Ala	Ser	Ser	Pro	Pro	
				905					910					915	
Ser	Pro	Arg	Asp	Glu	Ile	Phe	Leu	Thr	Pro	Asn	Leu	Ser	Leu	Pro	
				920					925					930	
Leu	Trp	Glu	Trp	Arg	Pro	Asp	Trp	Leu	Glu	Asp	Met	Glu	Val	Ser	
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His	Thr	Gln	Arg	Leu	Gly	Arg	Gly	Met	Pro	Pro	Trp	Pro	Pro	Asp	
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Ser	Gln	Ile	Ser	Ser	Gln	Arg	Ser	Gln	Leu	His	Cys	Arg	Met	Pro	
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<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 212

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<210> 213

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 213

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<210> 214

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 214

aggactacac ggagcctgtg gagcttctgg ctgtgcgaat tcagctggaa 50

<210> 215

<211> 2749

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 1869, 1887

<223> unknown base

<400> 215

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<211> 332  
<212> PRT  
<213> Homo sapiens

<400> 216  
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20 25 30  
Asp Thr Val Ser Leu Gln Cys Thr Tyr Arg Glu Glu Leu Arg Asp  
35 40 45  
His Arg Lys Tyr Trp Cys Arg Lys Gly Gly Ile Leu Phe Ser Arg  
50 55 60  
Cys Ser Gly Thr Ile Tyr Ala Glu Glu Gly Gln Glu Thr Met  
65 70 75  
Lys Gly Arg Val Ser Ile Arg Asp Ser Arg Gln Glu Leu Ser Leu  
80 85 90  
Ile Val Thr Leu Trp Asn Leu Thr Leu Gln Asp Ala Gly Glu Tyr  
95 100 105  
Trp Cys Gly Val Glu Lys Arg Gly Pro Asp Glu Ser Leu Leu Ile  
110 115 120  
Ser Leu Phe Val Phe Pro Gly Pro Cys Cys Pro Pro Ser Pro Ser  
125 130 135  
Pro Thr Phe Gln Pro Leu Ala Thr Thr Arg Leu Gln Pro Lys Ala  
140 145 150  
Lys Ala Gln Gln Thr Gln Pro Pro Gly Leu Thr Ser Pro Gly Leu  
155 160 165  
Tyr Pro Ala Ala Thr Thr Ala Lys Gln Gly Lys Thr Gly Ala Glu  
170 175 180  
Ala Pro Pro Leu Pro Gly Thr Ser Gln Tyr Gly His Glu Arg Thr  
185 190 195  
Ser Gln Tyr Thr Gly Thr Ser Pro His Pro Ala Thr Ser Pro Pro

200	205	210
Ala Gly Ser Ser Arg Pro Pro Met Gln	Leu Asp Ser Thr Ser Ala	
215	220	225
Glu Asp Thr Ser Pro Ala Leu Ser Ser	Gly Ser Ser Lys Pro Arg	
230	235	240
Val Ser Ile Pro Met Val Arg Ile Leu	Ala Pro Val Leu Val Leu	
245	250	255
Leu Ser Leu Leu Ser Ala Ala Gly Leu	Ile Ala Phe Cys Ser His	
260	265	270
Leu Leu Leu Trp Arg Lys Glu Ala Gln	Gln Ala Thr Glu Thr Gln	
275	280	285
Arg Asn Glu Lys Phe Trp Leu Ser Arg	Leu Thr Ala Glu Glu Lys	
290	295	300
Glu Ala Pro Ser Gln Ala Pro Glu Gly	Asp Val Ile Ser Met Pro	
305	310	315
Pro Leu His Thr Ser Glu Glu Glu Leu	Gly Phe Ser Lys Phe Val	
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Ser Ala

<210> 217

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 217

ccctgcagtg cacctacagg gaag 24

<210> 218

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 218

ctgtcttccc ctgcttggt gtgg 24

<210> 219

<211> 47

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 219  
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<210> 220  
 <211> 950  
 <212> DNA  
 <213> Homo sapiens

<400> 220  
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 cagtgtgaaa gaaccagtgg tctcgtctctg ttgccaggc tagagtgtac 150  
 tggcgtgac atagctcact gcagcctcag actcctggac ttgagaaatc 200  
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<210> 221  
 <211> 146  
 <212> PRT  
 <213> Homo sapiens

<400> 221  
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 1 5 10 15  
 Ser Glu Ala Lys Leu Tyr Gly Arg Cys Glu Leu Ala Arg Val Leu  
 20 25 30

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Trp	Val	Cys	Leu	Ala	Tyr	Phe	Thr	Ser	Gly	Phe	Asn	Ala	Ala	Ala	50	55	60
Leu	Asp	Tyr	Glu	Ala	Asp	Gly	Ser	Thr	Asn	Asn	Gly	Ile	Phe	Gln	65	70	75
Ile	Asn	Ser	Arg	Arg	Trp	Cys	Ser	Asn	Leu	Thr	Pro	Asn	Val	Pro	80	85	90
Asn	Val	Cys	Arg	Met	Tyr	Cys	Ser	Asp	Leu	Leu	Asn	Pro	Asn	Leu	95	100	105
Lys	Asp	Thr	Val	Ile	Cys	Ala	Met	Lys	Ile	Thr	Gln	Glu	Pro	Gln	110	115	120
Gly	Leu	Gly	Tyr	Trp	Glu	Ala	Trp	Arg	His	His	Cys	Gln	Gly	Lys	125	130	135
Asp	Leu	Thr	Glu	Trp	Val	Asp	Gly	Cys	Asp	Phe					140	145	

<210> 222

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 222

gggatcatgt tgttgccct ggtc 24

<210> 223

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 223

gcaaggcaga cccagtcagc cag 23

<210> 224

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 224

ctgcctgcta ccctccaagt gaggccaagc tctacggtcg ttgtg 45

<210> 225



<211> 2049  
<212> DNA  
<213> Homo sapiens

<400> 225

agccgctgcc ccgggcccggg cgcgcgcggc ggcacccatga gtccccgctc 50  
gtgcctgcgt tcgctgcgcc tcctcgtctt cgcctcttc tcagccgccg 100  
cgagcaactg gctgtacctg gccaaagctgt cgtcgggtggg gagcatctca 150  
gaggaggaga cgtgcgagaa actcaagggc ctgatccaga ggcaggtgca 200  
gatgtgcaag cggaacctgg aagtcattgga ctccgtgcgc cgcgggtgcc 250  
agctggccat tgaggagtgc cagtaccagt tccggaaccg gcgctggaac 300  
tgctccacac tcgactcctt gcccgctctt ggcaagggtg tgacgcaagg 350  
gactcgggag gcggccttcg tgtacgccat ctcttcggca ggtgtggcct 400  
ttgcagtgc gcgggcgtgc agcagtgggg agctggagaa gtgcggctgt 450  
gacaggacag tgcattgggt cagcccacag ggcttccagt ggtcaggatg 500  
ctctgacaac atcgccctac gtgtggcctt ctccagtcg tttgtggatg 550  
tgccgggagag aagcaagggg gcctcgtcca gcagagccct catgaacctc 600  
cacaacaatg aggccggcag gaaggccatc ctgacacaca tgcgggtgga 650  
atgcaagtgc cacgggggtgt caggctcctg tgaggtaaag acgtgctggc 700  
gagccgtgcc gcccttcgc cagggtgggtc acgcactgaa ggagaagttt 750  
gatggtgcca ctgagggtga gccacgccgc gtgggctcct ccagggcact 800  
ggtaccacgc aacgcacagt tcaagccgca cacagatgag gacctggtgt 850  
acttgagacc tagccccgac ttctgtgagc aggacatgcg cagcggcgtg 900  
ctgggcacga ggggccgcac atgcaacaag acgtccaagg ccatcgacgg 950  
ctgtgagctg ctgtgctgtg gccgcggctt ccacacggcg cagggtggagc 1000  
tggtgaacg ctgcagctgc aaattccact ggtgctgctt cgtcaagtgc 1050  
cggcagtgcc agcggctcgt ggagttgcac acgtgccgat gaccgcctgc 1100  
ctagccctgc gccggcaacc acctagtggc ccagggaagg ccgataattt 1150  
aaacagtctc ccaccaccta cccaagaga tactggttgt attttttgtt 1200  
ctggtttggt ttttgggtcc tcatgttatt tattgccgaa accaggcagg 1250  
caaccccaag ggcaccaacc agggcctccc caaagcctgg gcctttgtgg 1300  
ctgccactga ccaaaggac cttgctcgtg ccgctggctg cccgcatgtg 1350

gctgccactg accactcagt tggtatctgt gtccgttttt ctacttgcag 1400  
 acctaagggtg gagtaacaag gagtattacc accacatggc tactgaccgt 1450  
 gtcacgcggg aagagggggc cttatggcag ggaaaatagg taccgacttg 1500  
 atggaagtca caccctctgg aaaaaagaac tcttaactct ccagcacaca 1550  
 tacacatgga ctcttggcag cttgagccta gaagccatgt ctctcaaagt 1600  
 ccctgagaaa gggaacaagc agataccagg tcaagggcac caggttcatt 1650  
 tcagccctta catggacagc tagagggttcg atatctgtgg gtccttccag 1700  
 gcaagaagag ggagatgaga gcaagagacg actgaagtcc caccctagaa 1750  
 cccagcctgc cccagcctgc ccctgggaag aggaaactta accactcccc 1800  
 agaccacact aggcaggcat ataggctgcc atcctggacc agggatcccg 1850  
 gctgtgcctt tgcagtcag cccgagtcac ctttcacagc gctgttcctc 1900  
 catgaaactg aaaaacacac acacacacac acacacacac acacacacac 1950  
 acacacacac ggacacacac acacacctgc gagagagagg gaggaaaggg 2000  
 ctgtgccttt gcagtcagtc ccgagtcacc tttcacagca ctgttcctc 2049

<210> 226  
 <211> 351  
 <212> PRT  
 <213> Homo sapiens

<400> 226  
 Met Ser Pro Arg Ser Cys Leu Arg Ser Leu Arg Leu Leu Val Phe  
 1 5 10 15  
 Ala Val Phe Ser Ala Ala Ala Ser Asn Trp Leu Tyr Leu Ala Lys  
 20 25 30  
 Leu Ser Ser Val Gly Ser Ile Ser Glu Glu Glu Thr Cys Glu Lys  
 35 40 45  
 Leu Lys Gly Leu Ile Gln Arg Gln Val Gln Met Cys Lys Arg Asn  
 50 55 60  
 Leu Glu Val Met Asp Ser Val Arg Arg Gly Ala Gln Leu Ala Ile  
 65 70 75  
 Glu Glu Cys Gln Tyr Gln Phe Arg Asn Arg Arg Trp Asn Cys Ser  
 80 85 90  
 Thr Leu Asp Ser Leu Pro Val Phe Gly Lys Val Val Thr Gln Gly  
 95 100 105  
 Thr Arg Glu Ala Ala Phe Val Tyr Ala Ile Ser Ser Ala Gly Val  
 110 115 120

Ala	Phe	Ala	Val	Thr	Arg	Ala	Cys	Ser	Ser	Gly	Glu	Leu	Glu	Lys
				125					130					135
Cys	Gly	Cys	Asp	Arg	Thr	Val	His	Gly	Val	Ser	Pro	Gln	Gly	Phe
				140					145					150
Gln	Trp	Ser	Gly	Cys	Ser	Asp	Asn	Ile	Ala	Tyr	Gly	Val	Ala	Phe
				155					160					165
Ser	Gln	Ser	Phe	Val	Asp	Val	Arg	Glu	Arg	Ser	Lys	Gly	Ala	Ser
				170					175					180
Ser	Ser	Arg	Ala	Leu	Met	Asn	Leu	His	Asn	Asn	Glu	Ala	Gly	Arg
				185					190					195
Lys	Ala	Ile	Leu	Thr	His	Met	Arg	Val	Glu	Cys	Lys	Cys	His	Gly
				200					205					210
Val	Ser	Gly	Ser	Cys	Glu	Val	Lys	Thr	Cys	Trp	Arg	Ala	Val	Pro
				215					220					225
Pro	Phe	Arg	Gln	Val	Gly	His	Ala	Leu	Lys	Glu	Lys	Phe	Asp	Gly
				230					235					240
Ala	Thr	Glu	Val	Glu	Pro	Arg	Arg	Val	Gly	Ser	Ser	Arg	Ala	Leu
				245					250					255
Val	Pro	Arg	Asn	Ala	Gln	Phe	Lys	Pro	His	Thr	Asp	Glu	Asp	Leu
				260					265					270
Val	Tyr	Leu	Glu	Pro	Ser	Pro	Asp	Phe	Cys	Glu	Gln	Asp	Met	Arg
				275					280					285
Ser	Gly	Val	Leu	Gly	Thr	Arg	Gly	Arg	Thr	Cys	Asn	Lys	Thr	Ser
				290					295					300
Lys	Ala	Ile	Asp	Gly	Cys	Glu	Leu	Leu	Cys	Cys	Gly	Arg	Gly	Phe
				305					310					315
His	Thr	Ala	Gln	Val	Glu	Leu	Ala	Glu	Arg	Cys	Ser	Cys	Lys	Phe
				320					325					330
His	Trp	Cys	Cys	Phe	Val	Lys	Cys	Arg	Gln	Cys	Gln	Arg	Leu	Val
				335					340					345
Glu	Leu	His	Thr	Cys	Arg									
				350										

<210> 227

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 227

gctgcagctg caaattccac tgg 23

<210> 228  
 <211> 28  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 228  
 tggtagggaga ctgttttaaata tatcggcc 28

<210> 229  
 <211> 41  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 229  
 tgcttcgtca agtgccggca gtgccagcgg ctctgtggagt t 41

<210> 230  
 <211> 1355  
 <212> DNA  
 <213> Homo sapiens

<400> 230  
 cggacgcgtg ggccggacgcg tgggaggacg cgtggggcga cgcgtgggct 50  
 ggggtgcctgc atcgccatgg acaccaccag gtacagcaag tggggcggca 100  
 gctccgagga ggtccccgga gggccctggg gacgctgggt gcaactggagc 150  
 aggagacccc tcttcttggc cctggctgtc ctggtcacca cagtcccttg 200  
 ggctgtgatt ctgagtatcc tattgtccaa ggcctccacg gagcgcgcg 250  
 cgctgcttga cggccacgac ctgctgagga caaacgcctc gaagcagacg 300  
 gcggcgctgg gtgccctgaa ggaggaggtc ggagactgcc acagctgctg 350  
 ctcggggacg caggcgagc tgcagaccac gcgcgcggag cttggggagg 400  
 cgcaggcgaa gctgatggag caggagagcg ccctgcggga actgcgtgag 450  
 cgcgtgaccc agggcttggc tgaagccggc aggggcccgtg aggacgtccg 500  
 cactgagctg ttccgggagc tggaggccgt gaggctccag aacaactcct 550  
 gcgagccgtg cccacgctg tggctgtcct tcgagggtc ctgctacttt 600  
 ttctctgtgc caaagacgac gtgggagggc gcgcaggatc actgcgcaga 650  
 tgccagcgcg cacctggtga tcgttggggg cctggatgag cagggttcc 700  
 tcactcgga cgcgcgtggc cgtggttact ggctgggcct gagggctgtg 750

cgccatctgg gcaaggttca gggctaccag tgggtggacg gagtctctct 800  
cagcttcagc cactggaacc agggagagcc caatgacgct tgggggcgcg 850  
agaactgtgt catgatgctg cacacggggc tgtggaacga cgcaccgtgt 900  
gacagcgaga aggacggctg gatctgtgag aaaaggcaca actgctgacc 950  
ccgcccagtg ccttgagacc gcgcccattg cagcatgtcg ttcctgggg 1000  
gctgctcacc tcctggctc ctggagctga ttgccaaaga gtttttttct 1050  
tcctcatcca ccgctgctga gtctcagaaa cacttggccc aacatagccc 1100  
tgtccagccc agtgccctggg ctctgggacc tccatgcga cctcatccta 1150  
actccactca cgcagacca acctaacctc cactagctcc aaaatccctg 1200  
ctcctgcgtc cccgtgatat gcctccactt ctctccctaa ccaaggttag 1250  
gtgactgagg actggagctg tttggttttc tcgcattttc caccaaactg 1300  
gaagctgttt ttgcagcctg aggaagcatc aataaatatt tgagaaatga 1350  
aaaaa 1355

<210> 231  
<211> 293  
<212> PRT  
<213> Homo sapiens

<400> 231  
Met Asp Thr Thr Arg Tyr Ser Lys Trp Gly Gly Ser Ser Glu Glu  
1 5 10 15  
Val Pro Gly Gly Pro Trp Gly Arg Trp Val His Trp Ser Arg Arg  
20 25 30  
Pro Leu Phe Leu Ala Leu Ala Val Leu Val Thr Thr Val Leu Trp  
35 40 45  
Ala Val Ile Leu Ser Ile Leu Leu Ser Lys Ala Ser Thr Glu Arg  
50 55 60  
Ala Ala Leu Leu Asp Gly His Asp Leu Leu Arg Thr Asn Ala Ser  
65 70 75  
Lys Gln Thr Ala Ala Leu Gly Ala Leu Lys Glu Glu Val Gly Asp  
80 85 90  
Cys His Ser Cys Cys Ser Gly Thr Gln Ala Gln Leu Gln Thr Thr  
95 100 105  
Arg Ala Glu Leu Gly Glu Ala Gln Ala Lys Leu Met Glu Gln Glu  
110 115 120  
Ser Ala Leu Arg Glu Leu Arg Glu Arg Val Thr Gln Gly Leu Ala  
125 130 135

Glu	Ala	Gly	Arg	Gly	Arg	Glu	Asp	Val	Arg	Thr	Glu	Leu	Phe	Arg
				140					145					150
Ala	Leu	Glu	Ala	Val	Arg	Leu	Gln	Asn	Asn	Ser	Cys	Glu	Pro	Cys
				155					160					165
Pro	Thr	Ser	Trp	Leu	Ser	Phe	Glu	Gly	Ser	Cys	Tyr	Phe	Phe	Ser
				170					175					180
Val	Pro	Lys	Thr	Thr	Trp	Ala	Ala	Ala	Gln	Asp	His	Cys	Ala	Asp
				185					190					195
Ala	Ser	Ala	His	Leu	Val	Ile	Val	Gly	Gly	Leu	Asp	Glu	Gln	Gly
				200					205					210
Phe	Leu	Thr	Arg	Asn	Thr	Arg	Gly	Arg	Gly	Tyr	Trp	Leu	Gly	Leu
				215					220					225
Arg	Ala	Val	Arg	His	Leu	Gly	Lys	Val	Gln	Gly	Tyr	Gln	Trp	Val
				230					235					240
Asp	Gly	Val	Ser	Leu	Ser	Phe	Ser	His	Trp	Asn	Gln	Gly	Glu	Pro
				245					250					255
Asn	Asp	Ala	Trp	Gly	Arg	Glu	Asn	Cys	Val	Met	Met	Leu	His	Thr
				260					265					270
Gly	Leu	Trp	Asn	Asp	Ala	Pro	Cys	Asp	Ser	Glu	Lys	Asp	Gly	Trp
				275					280					285
Ile	Cys	Glu	Lys	Arg	His	Asn	Cys							
				290										

<210> 232  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 232  
 gcgagaactg tgtcatgatg ctgc 24

<210> 233  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 233  
 gttttctgaga ctcagcagcg gtgg 24

<210> 234  
 <211> 50  
 <212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 234

caccgtgtga cagcgagaag gacggctgga tctgtgagaa aaggcacaac 50

<210> 235

<211> 1847

<212> DNA

<213> Homo sapiens

<400> 235

gccaggggaa gaggggtgatc cgacccgggg aaggtcgctg ggcagggcga 50  
gttgggaaag cggcagcccc cgccgcccc gcagcccctt ctctccttt 100  
ctccacgctc ctatctgcct ctcgctggag gccaggcgt gcagcatcga 150  
agacaggagg aactggagcc tcattggccg gcccggggcg ccggcctcgg 200  
gcttaaatag gagctccggg ctctggctgg gaccgacccg ctgccggccg 250  
cgctcccgt gctcctgccg ggtgatggaa aaccccagcc cggccgccgc 300  
cctgggcaag gccctctgcg ctctcctcct ggccactctc ggcgccgccg 350  
gccagcctct tgggggagag tccatctgtt ccgccagagc cccggccaaa 400  
tacagcatca ccttcacggg caagtggagc cagacggcct tcccaagca 450  
gtaccccctg ttccgcccc ctgcgcagtg gtcttcgctg ctggggggccg 500  
cgcatagctc cgactacagc atgtggagga agaaccagta cgtcagtaac 550  
gggctgcgcg actttgcgga gcgcggcgag gcctgggcgc tgatgaagga 600  
gatcgaggcg gcgggggagg cgctgcagag cgtgcacgag gtgttttcgg 650  
cgcccgcgt cccagcggc accgggcaga cgtcggcgga gctggagggtg 700  
cagcgcaggc actcgctggt ctcgtttggt gtgcgcacgc tgcccagccc 750  
cgactggttc gtgggctggt acagcctgga cctgtgcgac ggggaccgtt 800  
ggcgggaaca ggcggcgctg gacctgtacc cctacgacgc cgggacggac 850  
agcggcttca ccttctctc cccaacttc gccaccatcc cgcaggacac 900  
ggtgaccgag ataacgtcct cctctcccag ccacccggcc aactccttct 950  
actaccgcg gctgaaggcc ctgcctccca tcgccagggt gacactgctg 1000  
cggctgcgac agagccccag ggccttcac cctcccgccc cagtctgcc 1050  
cagcagggac aatgagattg tagacagcgc ctacagttcca gaaacgccgc 1100

tggactgcga ggtctccctg tggctcgtcct ggggactgtg cggaggccac 1150  
 tgtgggagggc tcgggaccaa gagcaggact cgctacgtcc gggccagacc 1200  
 cgccaacaac gggagccoct gccccgagct cgaagaagag gctgagtgcg 1250  
 tccctgataa ctgcgtctaa gaccagagcc ccgcagcccc tggggccccc 1300  
 cggagccatg ggggtgtcggg ggctcctgtg caggctcatg ctgcaggcgg 1350  
 ccgagggcac aggggggtttc gcgctgctcc tgaccgcggt gaggccgcgc 1400  
 cgaccatctc tgcactgaag ggccctctgg tggccggcac gggcattggg 1450  
 aaacagcctc ctccctttccc aaccttgctt cttagggggc cccgtgtccc 1500  
 gtctgtctc agcctcctcc tcctgcagga taaagtcac cccaaggctc 1550  
 cagctactct aaattatgtc tccttataag ttattgctgc tccaggagat 1600  
 tgtccttcat cgtccagggg cctggctccc acgtgggtgc agatacctca 1650  
 gacctggtgc tctaggctgt gctgagccca ctctcccag ggcgcatcca 1700  
 agcggggggc acttgagaag tgaataaatg gggcggtttc ggaagcgtca 1750  
 gtgtttccat gttatggatc tctctgcgtt tgaataaaga ctatctctgt 1800  
 tgctcacaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaa 1847

<210> 236  
 <211> 331  
 <212> PRT  
 <213> Homo sapiens

<400> 236  
 Met Glu Asn Pro Ser Pro Ala Ala Ala Leu Gly Lys Ala Leu Cys  
 1 5 10 15  
 Ala Leu Leu Leu Ala Thr Leu Gly Ala Ala Gly Gln Pro Leu Gly  
 20 25 30  
 Gly Glu Ser Ile Cys Ser Ala Arg Ala Pro Ala Lys Tyr Ser Ile  
 35 40 45  
 Thr Phe Thr Gly Lys Trp Ser Gln Thr Ala Phe Pro Lys Gln Tyr  
 50 55 60  
 Pro Leu Phe Arg Pro Pro Ala Gln Trp Ser Ser Leu Leu Gly Ala  
 65 70 75  
 Ala His Ser Ser Asp Tyr Ser Met Trp Arg Lys Asn Gln Tyr Val  
 80 85 90  
 Ser Asn Gly Leu Arg Asp Phe Ala Glu Arg Gly Glu Ala Trp Ala  
 95 100 105  
 Leu Met Lys Glu Ile Glu Ala Ala Gly Glu Ala Leu Gln Ser Val



[illegible]

<210> 237

<211> 22

<212> DNA

<213> Artificial Sequence

 $\langle 220 \rangle$ 

<223> Synthetic oligonucleotide probe

<400> 237

cagcactgcc aggggaagag gg 22

<210> 238  
 <211> 18  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic oligonucleotide probe  
  
 <400> 238  
 caggactcgc tacgtccg 18  
  
 <210> 239  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic oligonucleotide probe  
  
 <400> 239  
 cagccccttc tcctcctttc tccc 24  
  
 <210> 240  
 <211> 25  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic oligonucleotide probe  
  
 <400> 240  
 gcagttatca gggacgcact cagcc 25  
  
 <210> 241  
 <211> 18  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic oligonucleotide probe  
  
 <400> 241  
 ccagcgagag gcagatag 18  
  
 <210> 242  
 <211> 23  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic oligonucleotide probe  
  
 <400> 242  
 cggtcaccgt gtcctgcggg atg 23  
  
 <210> 243  
 <211> 42  
 <212> DNA



aagtggagaa gaaatcagtc agccgcagtg aagagctcag aaaagaagca 1150  
agacaattaa aacgggaact cttagcagca aaacaaaaaa aagtagaaaa 1200  
tgcagcaaaa caagcagaaa aaagaagtga agaggaagaa gcccctccag 1250  
atggtgctgt tgccgaatac agaagagaaa agcaaaagta tgaagctttg 1300  
aggaagcaac agtcaaagaa ggggaacttcc cggaagatc agacccttgc 1350  
actgctgaac cagtttaaat ctaaactcac tcaagcaatt gctgaaacac 1400  
ctgaaaatga cattcctgaa acagaagtag aagatgatga aggatggatg 1450  
tcacatgtac ttcagtttga ggataaaagc agaaaagtga aagatgcaag 1500  
catgcaagac tcagatacat ttgaaatcta tgatcctcgg aatccagtga 1550  
ataaaagaag gaggaagaa agcaaaaagc tgatgagaga gaaaaaagaa 1600  
agaagataaa atgagaataa tgataaccag aacttgctgg aaatgtgcct 1650  
acaatggcct tgtaacagcc attgttccca acagcatcac ttaggggtgt 1700  
gaaaagaagt atttttgaac ctgttgtctg gttttgaaaa acaattatct 1750  
tgttttgcaa attgtggaat gatgtaagca aatgcttttg gttactggta 1800  
catgtgtttt ttcctagctg accttttata ttgctaaatc tgaaataaaa 1850  
taactttcct tccacaaaaa aaaaaaaaaa aaaaaaaaaa aaaa 1894

<210> 245  
<211> 472  
<212> PRT  
<213> Homo sapiens

<400> 245  
Met Ser Asn Ile Tyr Ile Gln Glu Pro Pro Thr Asn Gly Lys Val  
1 5 10 15  
Leu Leu Lys Thr Thr Ala Gly Asp Ile Asp Ile Glu Leu Trp Ser  
20 25 30  
Lys Glu Ala Pro Lys Ala Cys Arg Asn Phe Ile Gln Leu Cys Leu  
35 40 45  
Glu Ala Tyr Tyr Asp Asn Thr Ile Phe His Arg Val Val Pro Gly  
50 55 60  
Phe Ile Val Gln Gly Gly Asp Pro Thr Gly Thr Gly Ser Gly Gly  
65 70 75  
Glu Ser Ile Tyr Gly Ala Pro Phe Lys Asp Glu Phe His Ser Arg  
80 85 90  
Leu Arg Phe Asn Arg Arg Gly Leu Val Ala Met Ala Asn Ala Gly  
95 100 105

Ser	His	Asp	Asn	Gly	Ser	Gln	Phe	Phe	Phe	Thr	Leu	Gly	Arg	Ala	
				110						115				120	
Asp	Glu	Leu	Asn	Asn	Lys	His	Thr	Ile	Phe	Gly	Lys	Val	Thr	Gly	
				125					130					135	
Asp	Thr	Val	Tyr	Asn	Met	Leu	Arg	Leu	Ser	Glu	Val	Asp	Ile	Asp	
				140					145					150	
Asp	Asp	Glu	Arg	Pro	His	Asn	Pro	His	Lys	Ile	Lys	Ser	Cys	Glu	
				155					160					165	
Val	Leu	Phe	Asn	Pro	Phe	Asp	Asp	Ile	Ile	Pro	Arg	Glu	Ile	Lys	
				170					175					180	
Arg	Leu	Lys	Lys	Glu	Lys	Pro	Glu	Glu	Glu	Val	Lys	Lys	Leu	Lys	
				185					190					195	
Pro	Lys	Gly	Thr	Lys	Asn	Phe	Ser	Leu	Leu	Ser	Phe	Gly	Glu	Glu	
				200					205					210	
Ala	Glu	Glu	Glu	Glu	Glu	Glu	Val	Asn	Arg	Val	Ser	Gln	Ser	Met	
				215					220					225	
Lys	Gly	Lys	Ser	Lys	Ser	Ser	His	Asp	Leu	Leu	Lys	Asp	Asp	Pro	
				230					235					240	
His	Leu	Ser	Ser	Val	Pro	Val	Val	Glu	Ser	Glu	Lys	Gly	Asp	Ala	
				245					250					255	
Pro	Asp	Leu	Val	Asp	Asp	Gly	Glu	Asp	Glu	Ser	Ala	Glu	His	Asp	
				260					265					270	
Glu	Tyr	Ile	Asp	Gly	Asp	Glu	Lys	Asn	Leu	Met	Arg	Glu	Arg	Ile	
				275					280					285	
Ala	Lys	Lys	Leu	Lys	Lys	Asp	Thr	Ser	Ala	Asn	Val	Lys	Ser	Ala	
				290					295					300	
Gly	Glu	Gly	Glu	Val	Glu	Lys	Lys	Ser	Val	Ser	Arg	Ser	Glu	Glu	
				305					310					315	
Leu	Arg	Lys	Glu	Ala	Arg	Gln	Leu	Lys	Arg	Glu	Leu	Leu	Ala	Ala	
				320					325					330	
Lys	Gln	Lys	Lys	Val	Glu	Asn	Ala	Ala	Lys	Gln	Ala	Glu	Lys	Arg	
				335					340					345	
Ser	Glu	Glu	Glu	Glu	Ala	Pro	Pro	Asp	Gly	Ala	Val	Ala	Glu	Tyr	
				350					355					360	
Arg	Arg	Glu	Lys	Gln	Lys	Tyr	Glu	Ala	Leu	Arg	Lys	Gln	Gln	Ser	
				365					370					375	
Lys	Lys	Gly	Thr	Ser	Arg	Glu	Asp	Gln	Thr	Leu	Ala	Leu	Leu	Asn	
				380					385					390	
Gln	Phe	Lys	Ser	Lys	Leu	Thr	Gln	Ala	Ile	Ala	Glu	Thr	Pro	Glu	

395	400	405
Asn Asp Ile Pro Glu Thr Glu Val Glu	Asp Asp Glu Gly Trp Met	
410	415	420
Ser His Val Leu Gln Phe Glu Asp Lys	Ser Arg Lys Val Lys Asp	
425	430	435
Ala Ser Met Gln Asp Ser Asp Thr Phe	Glu Ile Tyr Asp Pro Arg	
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455	460	465
Arg Glu Lys Lys Glu Arg Arg		
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<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

<400> 246

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<223> Synthetic oligonucleotide probe

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<223> Synthetic oligonucleotide probe

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cagatggtgc tggtgccg 18

<210> 249

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<223> Synthetic oligonucleotide probe

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<220>
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cctctccgat taaaacgc 18

<210> 252
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<212> DNA
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<400> 252
gagaggactg gttgccatgg caaatgctgg ttctcatgat aatgg 45

<210> 253
<211> 2456
<212> DNA
<213> Homo sapiens

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catttcgcct tgctgacggc gtcgagccct ggccagacat gtccacaggg 150
ttctccttcg ggtccgggac tctgggctcc accaccgtgg ccgcgggcgg 200
gaccagcaca ggcggcggtt tctccttcgg aacgggaacg tctagcaacc 250
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acctgccact gggttcactc taggaggaac aaatacaggt gccttgca 400

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35 40 45  
Asn Leu Gly Ser Thr Ser Thr Pro Ala Thr Thr Ser Ala Pro Ser  
50 55 60  
Ser Gly Phe Gly Thr Gly Leu Phe Gly Ser Lys Pro Ala Thr Gly  
65 70 75  
Phe Thr Leu Gly Gly Thr Asn Thr Gly Ala Leu His Thr Lys Arg  
80 85 90  
Pro Gln Val Val Thr Lys Tyr Gly Thr Leu Gln Gly Lys Gln Met  
95 100 105  
His Val Gly Lys Thr Pro Ile Gln Val Phe Leu Gly Val Pro Phe  
110 115 120  
Ser Arg Pro Pro Leu Gly Ile Leu Arg Phe Ala Pro Pro Glu Pro  
125 130 135

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Gly	Trp	Ser	Leu	Ala	Leu	Ser	Pro	Gly	Trp	Ser	Ala	Val	Ala	Arg	155	160	165
Ser	Arg	Leu	Thr	Ala	Thr	Ser	Ala	Ser	Arg	Val	Gln	Ala	Ser	Leu	170	175	180
Leu	Pro	Gln	Pro	Leu	Ser	Val	Trp	Gly	Tyr	Arg	Cys	Leu	Gln	Glu	185	190	195
Ser	Trp	Gly	Gln	Leu	Ala	Ser	Met	Tyr	Val	Ser	Thr	Arg	Glu	Arg	200	205	210
Tyr	Lys	Trp	Leu	Arg	Phe	Ser	Glu	Asp	Cys	Leu	Tyr	Leu	Asn	Val	215	220	225
Tyr	Ala	Pro	Ala	Arg	Ala	Pro	Gly	Asp	Pro	Gln	Leu	Pro	Val	Met	230	235	240
Val	Trp	Phe	Pro	Gly	Gly	Ala	Phe	Ile	Val	Gly	Ala	Ala	Ser	Ser	245	250	255
Tyr	Glu	Gly	Ser	Asp	Leu	Ala	Ala	Arg	Glu	Lys	Val	Val	Leu	Val	260	265	270
Phe	Leu	Gln	His	Arg	Leu	Gly	Ile	Phe	Gly	Phe	Leu	Ser	Thr	Asp	275	280	285
Asp	Ser	His	Ala	Arg	Gly	Asn	Trp	Gly	Leu	Leu	Asp	Gln	Met	Ala	290	295	300
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Arg	Ala	Ile	Ser	Gln	Ser	Gly	Thr	Ala	Leu	Phe	Arg	Leu	Phe	Ile	350	355	360
Thr	Ser	Asn	Pro	Leu	Lys	Val	Ala	Lys	Lys	Val	Ala	His	Leu	Ala	365	370	375
Gly	Cys	Asn	His	Asn	Ser	Thr	Gln	Ile	Leu	Val	Asn	Cys	Leu	Arg	380	385	390
Ala	Leu	Ser	Gly	Thr	Lys	Val	Met	Arg	Val	Ser	Asn	Lys	Met	Arg	395	400	405
Phe	Leu	Gln	Leu	Asn	Phe	Gln	Arg	Asp	Pro	Glu	Glu	Ile	Ile	Trp	410	415	420
Ser	Met	Ser	Pro	Val	Val	Asp	Gly	Val	Val	Ile	Pro	Asp	Asp	Pro			

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Leu Gly Val Asn Asn Leu Glu Phe Asn Trp Leu Leu Pro Tyr Asn					
	455		460		465
Ile Thr Lys Glu Gln Val Pro Leu Val Val Glu Glu Tyr Leu Asp					
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Asn Val Asn Glu His Asp Trp Lys Met Leu Arg Asn Arg Met Met					
	485		490		495
Asp Ile Val Gln Asp Ala Thr Phe Val Tyr Ala Thr Leu Gln Thr					
	500		505		510
Ala His Tyr His Arg Glu Thr Pro Met Met Gly Ile Cys Pro Ala					
	515		520		525
Gly His Ala Thr Thr Arg Met Lys Ser Thr Cys Ser Trp Ile Leu					
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<220>

<223> Synthetic oligonucleotide probe

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<210> 256

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 256

ccacctcagg aagccgaaga tgcc 24

<210> 257

<211> 45

<212> DNA

<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

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<211> 544

<212> PRT

<213> Homo sapiens

<400> 259

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Val	Pro	Glu	Gly	Leu	Cys	Ile	Ser	Val	Pro	Cys	Ser	Phe	Ser	Tyr
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Pro	Arg	Gln	Asp	Trp	Thr	Gly	Ser	Thr	Pro	Ala	Tyr	Gly	Tyr	Trp
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Gln	Leu	Thr	Gly	Asp	Pro	Ala	Lys	Gly	Asn	Cys	Ser	Leu	Val	Ile
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Arg	Asp	Ala	Gln	Met	Gln	Asp	Glu	Ser	Gln	Tyr	Phe	Phe	Arg	Val
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Glu	Arg	Gly	Ser	Tyr	Val	Thr	Tyr	Asn	Phe	Met	Asn	Asp	Gly	Phe
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Phe	Leu	Lys	Val	Thr	Val	Leu	Ser	Phe	Thr	Pro	Arg	Pro	Gln	Asp
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Val	Ser	Ala	Gln	Arg	Thr	Val	Arg	Leu	Arg	Val	Ala	Tyr	Ala	Pro
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Arg	Asp	Leu	Val	Ile	Ser	Ile	Ser	Arg	Asp	Asn	Thr	Pro	Ala	Leu
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Glu	Pro	Gln	Pro	Gln	Gly	Asn	Val	Pro	Tyr	Leu	Glu	Ala	Gln	Lys
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Gly	Gln	Phe	Leu	Arg	Leu	Leu	Cys	Ala	Ala	Asp	Ser	Gln	Pro	Pro
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Ala	Thr	Leu	Ser	Trp	Val	Leu	Gln	Asn	Arg	Val	Leu	Ser	Ser	Ser
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His	Pro	Trp	Gly	Pro	Arg	Pro	Leu	Gly	Leu	Glu	Leu	Pro	Gly	Val
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Leu	Glu	Asn	Leu	Gly	Asn	Gly	Thr	Ser	Leu	Pro	Val	Leu	Glu	Gly	
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Arg	Leu	Ser	Trp	Thr	Gln	Arg	Gly	Gln	Val	Leu	Ser	Pro	Ser	Gln	
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His	Glu	Gly	Glu	Phe	Thr	Cys	His	Ala	Arg	His	Pro	Leu	Gly	Ser	
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Gln	His	Val	Ser	Leu	Ser	Leu	Ser	Val	His	Tyr	Lys	Lys	Gly	Leu	
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Ile	Ser	Thr	Ala	Phe	Ser	Asn	Gly	Ala	Phe	Leu	Gly	Ile	Gly	Ile	
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Thr	Ala	Leu	Leu	Phe	Leu	Cys	Leu	Ala	Leu	Ile	Ile	Met	Lys	Ile	
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Leu	Pro	Lys	Arg	Arg	Thr	Gln	Thr	Glu	Thr	Pro	Arg	Pro	Arg	Phe	
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Ser	Arg	His	Ser	Thr	Ile	Leu	Asp	Tyr	Ile	Asn	Val	Val	Pro	Thr	
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Ala	Gly	Pro	Leu	Ala	Gln	Lys	Arg	Asn	Gln	Lys	Ala	Thr	Pro	Asn	
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Ser	Pro	Arg	Thr	Pro	Pro	Pro	Pro	Gly	Ala	Pro	Ser	Pro	Glu	Ser	
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Lys	Lys	Asn	Gln	Lys	Lys	Gln	Tyr	Gln	Leu	Pro	Ser	Phe	Pro	Glu	
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Glu	Leu	His	Tyr	Ala	Thr	Leu	Asn	Phe	Pro	Gly	Val	Arg	Pro	Arg	
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 aatgtaggaa gatattaaaa gtagatgaga ggacacaaga tgtagtcgat 2650  
 ccttatgcga ttatatcatt atttacttag gaaagagtaa aaataccaaa 2700  
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<210> 264

<211> 772

<212> PRT

<213> Homo sapiens

<400> 264

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Leu	Trp	Pro	Cys	Leu	Gly	Ala	Thr	Glu	Asn	Ser	Gln	Thr	Lys	Lys
				20					25					30
Val	Lys	Gln	Pro	Val	Arg	Ser	His	Leu	Arg	Val	Lys	Arg	Gly	Trp
				35					40					45
Val	Trp	Asn	Gln	Phe	Phe	Val	Pro	Glu	Glu	Met	Asn	Thr	Thr	Ser
				50					55					60

His	His	Ile	Gly	Gln	Leu	Arg	Ser	Asp	Leu	Asp	Asn	Gly	Asn	Asn		65	70	75
Ser	Phe	Gln	Tyr	Lys	Leu	Leu	Gly	Ala	Gly	Ala	Gly	Ser	Thr	Phe		80	85	90
Ile	Ile	Asp	Glu	Arg	Thr	Gly	Asp	Ile	Tyr	Ala	Ile	Gln	Lys	Leu		95	100	105
Asp	Arg	Glu	Glu	Arg	Ser	Leu	Tyr	Ile	Leu	Arg	Ala	Gln	Val	Ile		110	115	120
Asp	Ile	Ala	Thr	Gly	Arg	Ala	Val	Glu	Pro	Glu	Ser	Glu	Phe	Val		125	130	135
Ile	Lys	Val	Ser	Asp	Ile	Asn	Asp	Asn	Glu	Pro	Lys	Phe	Leu	Asp		140	145	150
Glu	Pro	Tyr	Glu	Ala	Ile	Val	Pro	Glu	Met	Ser	Pro	Glu	Gly	Thr		155	160	165
Leu	Val	Ile	Gln	Val	Thr	Ala	Ser	Asp	Ala	Asp	Asp	Pro	Ser	Ser		170	175	180
Gly	Asn	Asn	Ala	Arg	Leu	Leu	Tyr	Ser	Leu	Leu	Gln	Gly	Gln	Pro		185	190	195
Tyr	Phe	Ser	Val	Glu	Pro	Thr	Thr	Gly	Val	Ile	Arg	Ile	Ser	Ser		200	205	210
Lys	Met	Asp	Arg	Glu	Leu	Gln	Asp	Glu	Tyr	Trp	Val	Ile	Ile	Gln		215	220	225
Ala	Lys	Asp	Met	Ile	Gly	Gln	Pro	Gly	Ala	Leu	Ser	Gly	Thr	Thr		230	235	240
Ser	Val	Leu	Ile	Lys	Leu	Ser	Asp	Val	Asn	Asp	Asn	Lys	Pro	Ile		245	250	255
Phe	Lys	Glu	Ser	Leu	Tyr	Arg	Leu	Thr	Val	Ser	Glu	Ser	Ala	Pro		260	265	270
Thr	Gly	Thr	Ser	Ile	Gly	Thr	Ile	Met	Ala	Tyr	Asp	Asn	Asp	Ile		275	280	285
Gly	Glu	Asn	Ala	Glu	Met	Asp	Tyr	Ser	Ile	Glu	Glu	Asp	Asp	Ser		290	295	300
Gln	Thr	Phe	Asp	Ile	Ile	Thr	Asn	His	Glu	Thr	Gln	Glu	Gly	Ile		305	310	315
Val	Ile	Leu	Lys	Lys	Lys	Val	Asp	Phe	Glu	His	Gln	Asn	His	Tyr		320	325	330
Gly	Ile	Arg	Ala	Lys	Val	Lys	Asn	His	His	Val	Pro	Glu	Gln	Leu		335	340	345
Met	Lys	Tyr	His	Thr	Glu	Ala	Ser	Thr	Thr	Phe	Ile	Lys	Ile	Gln				

	350		355		360
Val Glu Asp Val	Asp Glu Pro Pro Leu	Phe Leu Leu Pro Tyr Tyr			
	365	370			375
Val Phe Glu Val	Phe Glu Glu Thr Pro	Gln Gly Ser Phe Val Gly			
	380	385			390
Val Val Ser Ala	Thr Asp Pro Asp Asn	Arg Lys Ser Pro Ile Arg			
	395	400			405
Tyr Ser Ile Thr	Arg Ser Lys Val Phe	Asn Ile Asn Asp Asn Gly			
	410	415			420
Thr Ile Thr Thr	Ser Asn Ser Leu Asp	Arg Glu Ile Ser Ala Trp			
	425	430			435
Tyr Asn Leu Ser	Ile Thr Ala Thr Glu	Lys Tyr Asn Ile Glu Gln			
	440	445			450
Ile Ser Ser Ile	Pro Leu Tyr Val Gln	Val Leu Asn Ile Asn Asp			
	455	460			465
His Ala Pro Glu	Phe Ser Gln Tyr Tyr	Glu Thr Tyr Val Cys Glu			
	470	475			480
Asn Ala Gly Ser	Gly Gln Val Ile Gln	Thr Ile Ser Ala Val Asp			
	485	490			495
Arg Asp Glu Ser	Ile Glu Glu His His	Phe Tyr Phe Asn Leu Ser			
	500	505			510
Val Glu Asp Thr	Asn Asn Ser Ser Phe	Thr Ile Ile Asp Asn Gln			
	515	520			525
Asp Asn Thr Ala	Val Ile Leu Thr Asn	Arg Thr Gly Phe Asn Leu			
	530	535			540
Gln Glu Glu Pro	Val Phe Tyr Ile Ser	Ile Leu Ile Ala Asp Asn			
	545	550			555
Gly Ile Pro Ser	Leu Thr Ser Thr Asn	Thr Leu Thr Ile His Val			
	560	565			570
Cys Asp Cys Gly	Asp Ser Gly Ser Thr	Gln Thr Cys Gln Tyr Gln			
	575	580			585
Glu Leu Val Leu	Ser Met Gly Phe Lys	Thr Glu Val Ile Ile Ala			
	590	595			600
Ile Leu Ile Cys	Ile Met Ile Ile Phe	Gly Phe Ile Phe Leu Thr			
	605	610			615
Leu Gly Leu Lys	Gln Arg Arg Lys Gln	Ile Leu Phe Pro Glu Lys			
	620	625			630
Ser Glu Asp Phe	Arg Glu Asn Ile Phe	Gln Tyr Asp Asp Glu Gly			
	635	640			645

Gly	Gly	Glu	Glu	Asp	Thr	Glu	Ala	Phe	Asp	Ile	Ala	Glu	Leu	Arg	
				650					655					660	
Ser	Ser	Thr	Ile	Met	Arg	Glu	Arg	Lys	Thr	Arg	Lys	Thr	Thr	Ser	
				665					670					675	
Ala	Glu	Ile	Arg	Ser	Leu	Tyr	Arg	Gln	Ser	Leu	Gln	Val	Gly	Pro	
				680					685					690	
Asp	Ser	Ala	Ile	Phe	Arg	Lys	Phe	Ile	Leu	Glu	Lys	Leu	Glu	Glu	
				695					700					705	
Ala	Asn	Thr	Asp	Pro	Cys	Ala	Pro	Pro	Phe	Asp	Ser	Leu	Gln	Thr	
				710					715					720	
Tyr	Ala	Phe	Glu	Gly	Thr	Gly	Ser	Leu	Ala	Gly	Ser	Leu	Ser	Ser	
				725					730					735	
Leu	Glu	Ser	Ala	Val	Ser	Asp	Gln	Asp	Glu	Ser	Tyr	Asp	Tyr	Leu	
				740					745					750	
Asn	Glu	Leu	Gly	Pro	Arg	Phe	Lys	Arg	Leu	Ala	Cys	Met	Phe	Gly	
				755					760					765	
Ser	Ala	Val	Gln	Ser	Asn	Asn									
				770											

<210> 265  
 <211> 349  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> unsure  
 <222> 24, 60, 141, 226, 228, 249, 252  
 <223> unknown base

<400> 265  
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 gaatatatttn taaaatggat agagaactgc aagatgagta ttgggtaatc 100  
 attcaagcca aggacatgat tggtcagcca ggagcgttgt ntggaacaac 150  
 aagtgtatta attaaacttt cagatgttaa tgacaataag cctatatatta 200  
 aagaaagttt ataccgcttg actgtntntg aatctgcacc cactgggant 250  
 tntataggaa caatcatggc atatgataat gacataggag agaatgcaga 300  
 aatggattac agcattgaag aggatgattc gcaaacattt gacattatt 349

<210> 266  
 <211> 25  
 <212> DNA  
 <213> Artificial Sequence

<220>



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 gttcaagaat tctatgaccc tatgacccca gtcaatgcca ggtacgaatt 700  
 tggtcaggct ctcttcactg gctgggctgc tgcttctctc tgccttcttg 750  
 gaggtgccct actttgctgt tccgtgcccc gaaaaacaac ctcttaccca 800  
 acaccaaggc cctatccaaa acctgcacct tccagcggga aagactacgt 850  
 gtgacacaga ggcaaaagga gaaaatcatg ttgaaacaaa ccgaaaatgg 900  
 acattgagat actatcatta acattaggac cttagaattt tgggtattgt 950  
 aatctgaagt atgggtattac aaaacaaaca aacaaacaaa aaacccatgt 1000  
 gttaaaatac tcagtgctaa acatggctta atcttatttt atcttctttc 1050  
 ctcaatatag gagggaagat ttttccattt gtattactgc ttcccattga 1100  
 gtaatcatac tcaaatgggg gaaggggtgc tccttaaata tatatagata 1150  
 tgtatatata catgtttttc tattaanaat agacagtaaa atactattct 1200  
 cattatgttg atactagcat acttaaaata tctctaaaat aggtaaatgt 1250  
 atttaattcc atattgatga agatgtttat tgggtatatt tctttttcgt 1300  
 ccttatatac atatgtaaca gtcaaatac atttactctt cttcattagc 1350  
 tttgggtgcc tttgccacaa gacctagcct aatttaccaa ggatgaattc 1400  
 tttcaattct tcatgcgtgc ccttttcata tacttatttt attttttacc 1450  
 ataatcttat agcacttgca tcgttattaa gcccttattt gttttgtgtt 1500  
 tcattggctt ctatctcctg aatctaacac atttcatagc ctacatttta 1550  
 gtttctaaag ccaagaagaa tttattacaa atcagaactt tggaggcaaa 1600  
 tctttctgca tgaccaaaagt gataaattcc tgttgacctt cccacacaat 1650  
 ccctgtactc tgacccatag cactcttggt tgctttgaaa atatttgtcc 1700  
 aattgagtag ctgcatgctg ttccccaggg tgttgtaaca caactttatt 1750  
 gattgaattt ttaagctact tattcatagt tttatatccc cctaaactac 1800  
 ctttttggtc ccatttcctt aattgtattg ttttccaag tgaattatc 1850  
 atgcgtttta tatcttccta ataagggtgt gtctgtttgt ctgaacaaag 1900  
 tgctagactt tctggagtga taatctggtg acaaatttc tctctgtagc 1950  
 tgtaagcaag tcacttaatc tttctacctc ttttttctat ctgccaaatt 2000  
 gagataatga tacttaacca gttagaagag gtagtgtgaa tattaattag 2050





Ile Gly Gly Ala	Ile Phe Leu Leu Ala	Gly Leu Ala Ile Leu Val
125		130 135
Ala Thr Ala Trp	Tyr Gly Asn Arg Ile	Val Gln Glu Phe Tyr Asp
140		145 150
Pro Met Thr Pro	Val Asn Ala Arg Tyr	Glu Phe Gly Gln Ala Leu
155		160 165
Phe Thr Gly Trp	Ala Ala Ala Ser Leu	Cys Leu Leu Gly Gly Ala
170		175 180
Leu Leu Cys Cys	Ser Cys Pro Arg Lys	Thr Thr Ser Tyr Pro Thr
185		190 195
Pro Arg Pro Tyr	Pro Lys Pro Ala Pro	Ser Ser Gly Lys Asp Tyr
200		205 210

Val

<210> 271  
 <211> 564  
 <212> DNA  
 <213> Homo sapiens  
 <220>  
 <221> unsure  
 <222> 21, 69, 163, 434, 436, 444  
 <223> unknown base

<400> 271  
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 ctccctatgc tggcgacaac atcgtgaccg cccagcccat gtacgagggg 150  
 ctgtggatgt ccngcgtgtc gcagagcacc gggcagatcc agtgcaaagt 200  
 ctttgactcc ttgtgaatc tgagcagcac attgcaagca acccgtgcct 250  
 tgatgggtgt tggcatcctc ctgggagtga tagcaatctt tgtggccacc 300  
 gttggcatga agtgtatgaa gtgcttgga gacgatgagg tgcagaagat 350  
 gaggatggct gtcattgggg gcgcgatatt tcttcttgca ggtctggcta 400  
 ttttagttgc cacagcatgg tatggcaata gaancnttca acantttctat 450  
 gaccctatga cccagtgcaa tgccaggtac gaatttggtc aggctctctt 500  
 cactggctgg gctgctgctt ctctctgcct tctgggaggt gccctacttt 550  
 gctgttcctg tccc 564

<210> 272  
 <211> 498



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 ctgctgcttc tctctgcctt ctgggaggtg ccctactttg ctgttctgc 550  
 ga 552

<210> 274  
 <211> 526  
 <212> DNA  
 <213> Homo sapiens  
 <220>  
 <221> unsure  
 <222> 25, 50, 60, 123, 127, 370, 395, 397-398, 402-403, 405-407  
 <223> unknown base

<400> 274  
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 tggaggattn actcctatgc tggcgacaac atcgtgacc cccaggccat 100  
 ttaccgagg gctttggatg tcntgcntgt cgcagagcac cgggcagatc 150  
 ccagtgcaaa gtctttgact ccttgctgaa tctgagcagc acattgcaag 200  
 caaccgtgc cttgatggg ttggcatcct cctgggagtg atagcaacct 250  
 ttgtggccac cgttggcatg aagtgtatga agtgcttga agacgatgag 300  
 gtgccagaag atgaggatgg ctgtcattgg gggcgcgata tttcttggtg 350  
 caggctctggc tatttttagtn gccacagcat ggtatggcaa tagantnntt 400  
 cnnngnnntct atgaccctat gacccagtc aatgccaggt acgaatttg 450  
 tcaggctctc ttcactggct gggctgctgc ttctctctgc cttctgggag 500  
 gtgcctact ttgctgttcc tgtccc 526

<210> 275  
 <211> 398  
 <212> DNA  
 <213> Homo sapiens  
 <220>  
 <221> unsure  
 <222> 22, 61, 91, 144, 238-239, 262, 265-266, 271, 274  
 <223> unknown base

<400> 275  
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 gcagcacatt ncaagcaacc ccttgcccttg aaggtggttg ncatcccccc 100  
 tgggagtgaa tagcaatctt tgtggccacc gttggcatga agtntatgaa 150  
 gtgcttgga gacgatgagg tgcagaagat gaggatggct gtcattgggg 200



<210> 278  
<211> 542  
<212> DNA  
<213> Homo sapiens

<220>  
<221> unsure  
<222> 26, 43, 55, 77, 198, 361-362, 391-392, 396  
<223> unknown base

<400> 278  
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ttacncctat gctggcgaac aacatcntga ccgcccaggc catgtacgag 100  
gggctgtgga atgtcctgcg tgtcccagag caccgggcag atccagtgc 150  
aagtctttga ctcttgctg aatctgagca gcacattgca agcaacctg 200  
ccttgatggt ggttggcatc ctctgggag tgatagcaat ctttgtggcc 250  
accgttggca tgaagtgtg tgaagtgctt ggaagacgat gaggtgcaga 300  
agatgaggat ggctgtcatt gggggcgcg tatttcttct tgcaggctg 350  
gctattttag nngccacagc atggtatggc aatcagaccc nntcanaaac 400  
tctatgacc tatgaccca gtcaatgcca ggtacgaatt tggtcaggct 450  
ctcttcaactg gctgggctgc tgcttctctc tgccttctgg gaggtgccct 500  
actttgctgt tcctgtcccc gaaaaacaac ctcttacca cg 542

<210> 279  
<211> 548  
<212> DNA  
<213> Homo sapiens

<220>  
<221> unsure  
<222> 90, 115, 147, 228, 387  
<223> unknown base

<400> 279  
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ccatcgtcag cactgccctg ccccatggag gatttactcn tatgctggcg 100  
acaacatcgt gaccnccag gccatgtacg aggggctgtg gatgtcngcg 150  
tgtcgagag caccgggcag atccagtgc aagtctttga ctcttgctg 200  
aatctgagca gcacattgca agcaacctg ccttgatggt ggttggcatc 250  
ctcctgggag tgatagcaat ctttgtggcc accgttggca tgaagtgtat 300  
gaagtgcttg gaagacgatg aggtgcagaa gatgaggatg gctgtcattg 350

ggggcgcgat atttcttctt gcaggtcttg ctatttntag ttgccacagc 400  
 atggtatggc aatagaatcg ttcaagaatt ctatgaccct atgaccccag 450  
 tcaatgccag gtacgaattt ggtcaggctc ttttactgg ctgggctgct 500  
 gcttctctct gccttctggg aggtgcccta ctttctgtt cctgcgaa 548

<210> 280  
 <211> 21  
 <212> DNA  
 <213> Artificial Sequence

<220> .  
 <223> Synthetic oligonucleotide probe

<400> 280  
 cgagcgagtc atggccaacg c 21

<210> 281  
 <211> 26  
 <212> DNA  
 <213> Artificial Sequence

<220> .  
 <223> Synthetic oligonucleotide probe

<400> 281  
 gtgtcacacg tagtctttcc cgctgg 26

<210> 282  
 <211> 43  
 <212> DNA  
 <213> Artificial Sequence

<220> .  
 <223> Synthetic oligonucleotide probe

<400> 282  
 ctgcagctgt tgggcttcat tctgccttc ctgggatgga tcg 43

<210> 283  
 <211> 2285  
 <212> DNA  
 <213> Homo sapiens

<400> 283  
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 ctgcgcctgc accgcgtaga ccgaccccc cctccagcgc gccacccgg 100  
 tagaggaccc ccgcccgtgc ccgaccggt cccgccttt ttgtaaaact 150  
 taaagcgggc gcagcattaa cgcttcccgc cccggtgacc tctcaggggt 200  
 ctccccgcca aaggtgctcc gccgctaagg aacatggcga aggtggagca 250  
 ggtcctgagc ctcgagccgc agcacgagct caaattccga ggtcccttca 300

ccgatgttgt caccaccaac ctaaagcttg gcaacccgac agaccgaaat 350  
gtgtgtttta aggtgaagac tacagcacca cgtaggtact gtgtgaggcc 400  
caacagcggga atcatcgatg caggggcctc aattaatgta tctgtgatgt 450  
tacagccttt cgattatgat cccaatgaga aaagtaaaca caagtttatg 500  
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gaaggaggca aaaccggaag accttatgga ttcaaaactt agatgtgtgt 600  
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acgtggccca ctcccgccc aggtgcttt ccgtgtcttc agttctgtcc 1450  
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gcgagggcac cagcagttgt ggggtggggag caagggaaga gagaaactct 2150  
tcagcgaatc cttctagtag tagttgagag tttgactgtg aattaatttt 2200  
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<210> 284  
<211> 243  
<212> PRT  
<213> Homo sapiens

<400> 284  
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20 25 30  
Lys Leu Gly Asn Pro Thr Asp Arg Asn Val Cys Phe Lys Val Lys  
35 40 45  
Thr Thr Ala Pro Arg Arg Tyr Cys Val Arg Pro Asn Ser Gly Ile  
50 55 60  
Ile Asp Ala Gly Ala Ser Ile Asn Val Ser Val Met Leu Gln Pro  
65 70 75  
Phe Asp Tyr Asp Pro Asn Glu Lys Ser Lys His Lys Phe Met Val  
80 85 90  
Gln Ser Met Phe Ala Pro Thr Asp Thr Ser Asp Met Glu Ala Val  
95 100 105  
Trp Lys Glu Ala Lys Pro Glu Asp Leu Met Asp Ser Lys Leu Arg  
110 115 120  
Cys Val Phe Glu Leu Pro Ala Glu Asn Asp Lys Pro His Asp Val  
125 130 135  
Glu Ile Asn Lys Ile Ile Ser Thr Thr Ala Ser Lys Thr Glu Thr  
140 145 150





<223> unknown base

<400> 286

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 gggagctgga gccccagcat gctggggagt gcggtcagct ccacacagta 150  
 gtcccccagc ggcccactcc cggcccaggc tgctttccgt gtcttcagtt 200  
 ctgtccaagc catcagctcc ttgggactga tgaacagagt cagaagccca 250  
 aaggaattgc cactgtggca gcatcagacg tactcgatcat aagtgaagg 300  
 cgtgtgttga ctgattgacc cagcgctttg gaaataaatg gcagtgcctt 350  
 gttcacttaa agggaccaag cttaaattga ttggttcatg tagtgaagtc 400  
 aaactgttat tcagagatgt ttaatgcata ttttaacttat ttaatgtatt 450  
 tcatctcatg ttttcttatt gtcacaagag tacagttaat gctgcgtgct 500  
 gctgaactct gttgggtgaa ctggtattgc tgctggaggg ctg 543

<210> 287

<211> 270

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 38, 64, 72, 164, 198, 200, 220, 222, 229, 242

<223> unknown base

<400> 287

ccctggtggt tttgttcttt aattcgttgg tgtaattntt gggaagattg 50  
 cttgtagagg tagnatgcac cnggctggta aattggattg gtggatccac 100  
 catatccatg ggattttaat ttatcataac catgtgtaaa aagaaattaa 150  
 tgtatgatga catntcacag gtattgcctt taaattaccc atccctgnan 200  
 acacatacac agatacacan anacaaatnt aatgtaacga tnttttagaa 250  
 agttaaaaaat gtatagtaac 270

<210> 288

<211> 428

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 35, 116, 129, 197, 278, 294, 297, 349, 351

<223> unknown base

<400> 288  
 ggtggcccat tcccggccca ggctgctttc cggtnnttcag ttctgtccaa 50  
 gccatcagct ccttgggact gatgaacaga gtcagaagcc caaaggaatt 100  
 gcactgtggc agcatnagac gtacttgtna taagtgagag gcgtgtgttg 150  
 actgattgac ccagcgcttt ggaaataaat ggcagtgcct tgttcantta 200  
 aaggggacca gctaaatttg tattggttca tgtagtgaag tcaaactggt 250  
 attcagagat gtttaatgca tatttaantt atttaatgta tttnatntca 300  
 tgttttctta ttgtcacaag agtacagtta atgctgcgtg ctgctgaant 350  
 ntgttgggtg aactgggtatt gctgctggag ggctgtgggc tcctctgtct 400  
 ttggagagtc tggatcatgtg gaggtggg 428

<210> 289  
 <211> 320  
 <212> DNA  
 <213> Homo sapiens

<400> 289  
 tgctttccgt gtcttcagtt ctgtccaagc catcagctcc ttgggacttg 50  
 atgaacagag tcagaagccc aaaggaattg cactgtggca gcatcagacg 100  
 tactcgatcat aagtgaagagg cgtgtgttga ctgattgacc cagcgctttg 150  
 gaaataaatg gcagtgcctt gttcacttaa agggaccaag cttaaatttg 200  
 attggttcat gtagtgaagt caaactgtta ttcagagatg tttaatgcat 250  
 atttaactta tttaatgtat ttcatctcat gttttcttat tgtcacaaga 300  
 gtacagttaa tgctgcgtgc 320

<210> 290  
 <211> 609  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> unsure  
 <222> 57, 60, 186, 235, 244, 304, 339, 355, 359, 361, 387, 432, 441,  
 447, 481, 513, 532, 584, 598  
 <223> unknown base

<400> 290  
 aaacctttta aagttgaggg gaaaagaatg atcctttatt aatgacaagg 50  
 gaaaccontgn gtaatgccac aatggcatat tgtaaatgtc attttaaaca 100  
 ttggtaggcc ttggtacatg atgctggatt acctctctta aaatgacacc 150  
 cttoctogcc tgttgggtgct ggcccttggg gagctngagc ccagcatgct 200

ggggagtgcg gtctgctcca cacagtagtc cccangtggc ccantcccgg 250  
 cccaggctgc tttccgtgtc ttcagttctg tccaagccat cagctccttg 300  
 ggantgatga acagagtcag aagcccaaag gaattgcant gtggcagcat 350  
 cagangtant ngtcataagt gagaggcgtg tgttgantga ttgaccacgc 400  
 gctttggaaa taaatggcag tgctttgttc anttaaaggg nccaagntaa 450  
 atttgtattg gttcatgtag tgaagtcaaa ntgttattca gagatgttta 500  
 atgcatattt aanttattta atgtatttca tntcatgttt tcttattgtc 550  
 acaagggtag agttaatgct gcgtgctgct gaantctgtt gggatgaantg 600  
 gtattgctg 609

<210> 291  
 <211> 493  
 <212> DNA  
 <213> Homo sapiens

<400> 291  
 ggcccttggg gagctggagc ccagcatgct ggggagtgcg gtcagctcca 50  
 cacagtagtc cccacgtggc ccaactccgg cccaggctgc tttccgtgtc 100  
 ttcagttctg tccaagccat cagctccttg ggactgatga acagagtcag 150  
 aagcccaaag gaattgcact gtggcagcat cagacgtact cgtcataagt 200  
 gagaggcgtg tgttgactga ttgaccacgc gctttggaaa taaatggcag 250  
 tgctttgttc acttaaaggg accaagctaa atttgtattg gttcatgtag 300  
 tgaagtcaaa ctgttattca gagatgttta atgcatattt aacttattta 350  
 atgtatttca tctcatgttt tcttattgtc acaagagtag agttaatgct 400  
 gcgtgctgct gaactctgtt gggatgaactg gtattgctgc tggagggctg 450  
 tgggctcctc tgtctctgga gactctggc atgtggaggt ggg 493

<210> 292  
 <211> 27  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 292  
 gcaccaccgt aggtacttgt gtgaggc 27

<210> 293  
 <211> 23  
 <212> DNA





```
cttcacaaat tatgaatgat catgtgttga aagccacatt attttatgct 2350
atacattcta tgtatgaggt gctacatttt taggacaaag aattctgtaa 2400
tctttttcaa gaaagagtct ttttctcctt gacaaaatcc agcttttgta 2450
tgaggactat aggggtgaatt ctctgattag taattttaga tatgtccttt 2500
cctaaaaaatg aataaaattt atgaatatga 2530
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```
<210> 296
<211> 413
<212> PRT
<213> Homo sapiens
```

<400> 296														
Met 1	Glu	Asn	Met	Leu 5	Leu	Trp	Leu	Ile	Phe 10	Phe	Thr	Pro	Gly	Trp 15
Thr	Leu	Ile	Asp	Gly 20	Ser	Glu	Met	Glu	Trp 25	Asp	Phe	Met	Trp	His 30
Leu	Arg	Lys	Val	Pro 35	Arg	Ile	Val	Ser	Glu 40	Arg	Thr	Phe	His	Leu 45
Thr	Ser	Pro	Ala	Phe 50	Glu	Ala	Asp	Ala	Lys 55	Met	Met	Val	Asn	Thr 60
Val	Cys	Gly	Ile	Glu 65	Cys	Gln	Lys	Glu	Leu 70	Pro	Thr	Pro	Ser	Leu 75
Ser	Glu	Leu	Glu	Asp 80	Tyr	Leu	Ser	Tyr	Glu 85	Thr	Val	Phe	Glu	Asn 90
Gly	Thr	Arg	Thr	Leu 95	Thr	Arg	Val	Lys	Val 100	Gln	Asp	Leu	Val	Leu 105
Glu	Pro	Thr	Gln	Asn 110	Ile	Thr	Thr	Lys	Gly 115	Val	Ser	Val	Arg	Arg 120
Lys	Arg	Gln	Val	Tyr 125	Gly	Thr	Asp	Ser	Arg 130	Phe	Ser	Ile	Leu	Asp 135
Lys	Arg	Phe	Leu	Thr 140	Asn	Phe	Pro	Phe	Ser 145	Thr	Ala	Val	Lys	Leu 150
Ser	Thr	Gly	Cys	Ser 155	Gly	Ile	Leu	Ile	Ser 160	Pro	Gln	His	Val	Leu 165
Thr	Ala	Ala	His	Cys 170	Val	His	Asp	Gly	Lys 175	Asp	Tyr	Val	Lys	Gly 180
Ser	Lys	Lys	Leu	Arg 185	Val	Gly	Leu	Leu	Lys 190	Met	Arg	Asn	Lys	Ser 195
Gly	Gly	Lys	Lys	Arg 200	Arg	Gly	Ser	Lys	Arg 205	Ser	Arg	Arg	Glu	Ala 210

Ser	Gly	Gly	Asp	Gln	Arg	Glu	Gly	Thr	Arg	Glu	His	Leu	Gln	Glu
				215					220					225
Arg	Ala	Lys	Gly	Gly	Arg	Arg	Arg	Lys	Lys	Ser	Gly	Arg	Gly	Gln
				230					235					240
Arg	Ile	Ala	Glu	Gly	Arg	Pro	Ser	Phe	Gln	Trp	Thr	Arg	Val	Lys
				245					250					255
Asn	Thr	His	Ile	Pro	Lys	Gly	Trp	Ala	Arg	Gly	Gly	Met	Gly	Asp
				260					265					270
Ala	Thr	Leu	Asp	Tyr	Asp	Tyr	Ala	Leu	Leu	Glu	Leu	Lys	Arg	Ala
				275					280					285
His	Lys	Lys	Lys	Tyr	Met	Glu	Leu	Gly	Ile	Ser	Pro	Thr	Ile	Lys
				290					295					300
Lys	Met	Pro	Gly	Gly	Met	Ile	His	Phe	Ser	Gly	Phe	Asp	Asn	Asp
				305					310					315
Arg	Ala	Asp	Gln	Leu	Val	Tyr	Arg	Phe	Cys	Ser	Val	Ser	Asp	Glu
				320					325					330
Ser	Asn	Asp	Leu	Leu	Tyr	Gln	Tyr	Cys	Asp	Ala	Glu	Ser	Gly	Ser
				335					340					345
Thr	Gly	Ser	Gly	Val	Tyr	Leu	Arg	Leu	Lys	Asp	Pro	Asp	Lys	Lys
				350					355					360
Asn	Trp	Lys	Arg	Lys	Ile	Ile	Ala	Val	Tyr	Ser	Gly	His	Gln	Trp
				365					370					375
Val	Asp	Val	His	Gly	Val	Gln	Lys	Asp	Tyr	Asn	Val	Ala	Val	Arg
				380					385					390
Ile	Thr	Pro	Leu	Lys	Tyr	Ala	Gln	Ile	Cys	Leu	Trp	Ile	His	Gly
				395					400					405
Asn	Asp	Ala	Asn	Cys	Ala	Tyr	Gly							
				410										

<210> 297  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 297  
 gcatctgcag gagagagcga aggg 24

<210> 298  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence



<220>  
<223> Synthetic oligonucleotide probe

<400> 298  
catcggtccc gtgaatccag aggc 24

<210> 299  
<211> 45  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 299  
gaaggagggc cttcctttca gtggacccgg gtcaagaata cccac 45

<210> 300  
<211> 1869  
<212> DNA  
<213> Homo sapiens

<400> 300  
aatgtgagag gggctgatgg aagctgatag gcaggactgg agtgtttagca 50  
ccagtactgg atgtgacagc aggcagagga gcacttagca gcttattcag 100  
tgtccgattc tgattccggc aaggatccaa gcatggaatg ctgccgtcgg 150  
gcaactcctg gcacactgct cctctttctg gctttcctgc tcctgagttc 200  
caggaccgca cgctccgagg aggaccggga cggcctatgg gatgcctggg 250  
gcccattggag tgaatgctca cgcacctgcg ggggaggggc ctccctactct 300  
ctgaggcgct gcctgagcag caagagctgt gaaggaagaa atatccgata 350  
cagaacatgc agtaatgtgg actgcccacc agaagcaggt gatttccgag 400  
ctcagcaatg ctcagctcat aatgatgtca agcaccatgg ccagttttat 450  
gaatggcttc ctgtgtctaa tgaccctgac aacctatgtt cactcaagtg 500  
ccaagccaaa ggaacaaccc tggttgttga actagcacct aaggtcttag 550  
atggtacgcg ttgctataca gaatctttgg atatgtgcat cagtggttta 600  
tgccaaattg ttggctgcga tcaccagctg ggaagcaccg tcaaggaaga 650  
taactgtggg gtctgcaacg gagatgggtc cacctgccgg ctggtccgag 700  
ggcagtataa atcccagctc tccgcaacca aatcggatga tactgtgggt 750  
gcacttcctt atggaagtag acatattcgc cttgtcttaa aaggtcctga 800  
tcacttatat ctggaaacca aaacctcca ggggactaaa ggtgaaaaca 850  
gtctcagctc cacaggaact ttccttgtgg acaattctag tgtggacttc 900



Leu	Ser	Ser	Lys	Ser	Cys	Glu	Gly	Arg	Asn	Ile	Arg	Tyr	Arg	Thr		65	70	75
Cys	Ser	Asn	Val	Asp	Cys	Pro	Pro	Glu	Ala	Gly	Asp	Phe	Arg	Ala		80	85	90
Gln	Gln	Cys	Ser	Ala	His	Asn	Asp	Val	Lys	His	His	Gly	Gln	Phe		95	100	105
Tyr	Glu	Trp	Leu	Pro	Val	Ser	Asn	Asp	Pro	Asp	Asn	Pro	Cys	Ser		110	115	120
Leu	Lys	Cys	Gln	Ala	Lys	Gly	Thr	Thr	Leu	Val	Val	Glu	Leu	Ala		125	130	135
Pro	Lys	Val	Leu	Asp	Gly	Thr	Arg	Cys	Tyr	Thr	Glu	Ser	Leu	Asp		140	145	150
Met	Cys	Ile	Ser	Gly	Leu	Cys	Gln	Ile	Val	Gly	Cys	Asp	His	Gln		155	160	165
Leu	Gly	Ser	Thr	Val	Lys	Glu	Asp	Asn	Cys	Gly	Val	Cys	Asn	Gly		170	175	180
Asp	Gly	Ser	Thr	Cys	Arg	Leu	Val	Arg	Gly	Gln	Tyr	Lys	Ser	Gln		185	190	195
Leu	Ser	Ala	Thr	Lys	Ser	Asp	Asp	Thr	Val	Val	Ala	Leu	Pro	Tyr		200	205	210
Gly	Ser	Arg	His	Ile	Arg	Leu	Val	Leu	Lys	Gly	Pro	Asp	His	Leu		215	220	225
Tyr	Leu	Glu	Thr	Lys	Thr	Leu	Gln	Gly	Thr	Lys	Gly	Glu	Asn	Ser		230	235	240
Leu	Ser	Ser	Thr	Gly	Thr	Phe	Leu	Val	Asp	Asn	Ser	Ser	Val	Asp		245	250	255
Phe	Gln	Lys	Phe	Pro	Asp	Lys	Glu	Ile	Leu	Arg	Met	Ala	Gly	Pro		260	265	270
Leu	Thr	Ala	Asp	Phe	Ile	Val	Lys	Ile	Arg	Asn	Ser	Gly	Ser	Ala		275	280	285
Asp	Ser	Thr	Val	Gln	Phe	Ile	Phe	Tyr	Gln	Pro	Ile	Ile	His	Arg		290	295	300
Trp	Arg	Glu	Thr	Asp	Phe	Phe	Pro	Cys	Ser	Ala	Thr	Cys	Gly	Gly		305	310	315
Gly	Tyr	Gln	Leu	Thr	Ser	Ala	Glu	Cys	Tyr	Asp	Leu	Arg	Ser	Asn		320	325	330
Arg	Val	Val	Ala	Asp	Gln	Tyr	Cys	His	Tyr	Tyr	Pro	Glu	Asn	Ile		335	340	345
Lys	Pro	Lys	Pro	Lys	Leu	Gln	Glu	Cys	Asn	Leu	Asp	Pro	Cys	Pro				

350	355	360
Ala Ser Asp Gly Tyr Lys Gln Ile Met	Pro Tyr Asp Leu Tyr His	
365	370	375
Pro Leu Pro Arg Trp Glu Ala Thr Pro	Trp Thr Ala Cys Ser Ser	
380	385	390
Ser Cys Gly Gly Gly Ile Gln Ser Arg	Ala Val Ser Cys Val Glu	
395	400	405
Glu Asp Ile Gln Gly His Val Thr Ser	Val Glu Glu Trp Lys Cys	
410	415	420
Met Tyr Thr Pro Lys Met Pro Ile Ala	Gln Pro Cys Asn Ile Phe	
425	430	435
Asp Cys Pro Lys Trp Leu Ala Gln Glu	Trp Ser Pro Cys Thr Val	
440	445	450
Thr Cys Gly Gln Gly Leu Arg Tyr Arg	Val Val Leu Cys Ile Asp	
455	460	465
His Arg Gly Met His Thr Gly Gly Cys	Ser Pro Lys Thr Lys Pro	
470	475	480
His Ile Lys Glu Glu Cys Ile Val Pro	Thr Pro Cys Tyr Lys Pro	
485	490	495
Lys Glu Lys Leu Pro Val Glu Ala Lys	Leu Pro Trp Phe Lys Gln	
500	505	510
Ala Gln Glu Leu Glu Glu Gly Ala Ala	Val Ser Glu Glu Pro Ser	
515	520	525

<210> 302  
 <211> 1533  
 <212> DNA  
 <213> Homo sapiens

<400> 302  
 cggacgcgtg ggcggcggct gcggaactcc cgtggagggg ccggtgggccc 50  
 ctcgggcctg acagatggca gtggccactg cggcggcagt actggccgct 100  
 ctgggcgggg cgctgtggct ggcgccccgc cggttcgtgg ggcccagggt 150  
 ccagcggctg cgagaggcg gggaccccg cctcatgcac ggggaagactg 200  
 tgctgatcac cggggcgaac agcggcctgg gccgcgccac ggccgcccag 250  
 ctactgcgcc tgggagcgcg ggtgatcatg ggctgccggg accgcgcgcg 300  
 cgccgaggag gcggcggtc agctccgccc cgagctccgc caggccgcgg 350  
 agtgcgggcc agagcctggc gtcagcggg tgggcgagct catagtccgg 400  
 gagctggacc tcgcctcgct gcgctcgtg cgcgccttct gccaggaaat 450



Val	Leu	Ile	Thr	Gly	Ala	Asn	Ser	Gly	Leu	Gly	Arg	Ala	Thr	Ala		50	55	60
Ala	Glu	Leu	Leu	Arg	Leu	Gly	Ala	Arg	Val	Ile	Met	Gly	Cys	Arg		65	70	75
Asp	Arg	Ala	Arg	Ala	Glu	Glu	Ala	Ala	Gly	Gln	Leu	Arg	Arg	Glu		80	85	90
Leu	Arg	Gln	Ala	Ala	Glu	Cys	Gly	Pro	Glu	Pro	Gly	Val	Ser	Gly		95	100	105
Val	Gly	Glu	Leu	Ile	Val	Arg	Glu	Leu	Asp	Leu	Ala	Ser	Leu	Arg		110	115	120
Ser	Val	Arg	Ala	Phe	Cys	Gln	Glu	Met	Leu	Gln	Glu	Glu	Pro	Arg		125	130	135
Leu	Asp	Val	Leu	Ile	Asn	Asn	Ala	Gly	Ile	Phe	Gln	Cys	Pro	Tyr		140	145	150
Met	Lys	Thr	Glu	Asp	Gly	Phe	Glu	Met	Gln	Phe	Gly	Val	Asn	His		155	160	165
Leu	Gly	His	Phe	Leu	Leu	Thr	Asn	Leu	Leu	Leu	Gly	Leu	Leu	Lys		170	175	180
Ser	Ser	Ala	Pro	Ser	Arg	Ile	Val	Val	Val	Ser	Ser	Lys	Leu	Tyr		185	190	195
Lys	Tyr	Gly	Asp	Ile	Asn	Phe	Asp	Asp	Leu	Asn	Ser	Glu	Gln	Ser		200	205	210
Tyr	Asn	Lys	Ser	Phe	Cys	Tyr	Ser	Arg	Ser	Lys	Leu	Ala	Asn	Ile		215	220	225
Leu	Phe	Thr	Arg	Glu	Leu	Ala	Arg	Arg	Leu	Glu	Gly	Thr	Asn	Val		230	235	240
Thr	Val	Asn	Val	Leu	His	Pro	Gly	Ile	Val	Arg	Thr	Asn	Leu	Gly		245	250	255
Arg	His	Ile	His	Ile	Pro	Leu	Leu	Val	Lys	Pro	Leu	Phe	Asn	Leu		260	265	270
Val	Ser	Trp	Ala	Phe	Phe	Lys	Thr	Pro	Val	Glu	Gly	Ala	Gln	Thr		275	280	285
Ser	Ile	Tyr	Leu	Ala	Ser	Ser	Pro	Glu	Val	Glu	Gly	Val	Ser	Gly		290	295	300
Arg	Tyr	Phe	Gly	Asp	Cys	Lys	Glu	Glu	Glu	Leu	Leu	Pro	Lys	Ala		305	310	315
Met	Asp	Glu	Ser	Val	Ala	Arg	Lys	Leu	Trp	Asp	Ile	Ser	Glu	Val		320	325	330
Met	Val	Gly	Leu	Leu	Lys													

<210> 304  
 <211> 521  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> unsure  
 <222> 20, 34, 62, 87, 221, 229  
 <223> unknown base

<400> 304  
 ggggattgta aagaggaagn actgtgccca aagntatgga tgaatctgtt 50  
 gcaagaaaat tntgggatat cagtgaagtg atggttngcc tgctaaaata 100  
 ggaacaagga gttaaagagc tgtttataaa actgcatatc agttatatct 150  
 gtgatcagga atggtgtgga ttgagaactt gttacttgaa gaaaaagaat 200  
 tttgatattg gaatagcctg ntaagaggna catgtgggta ttttggagtt 250  
 actgaaaaat ttttttggg ataagagaat ttcagcaaag atgtttttaa 300  
 tatatatagt aagtataatg aataataagt acaatgaaaa atacaattat 350  
 attgtaaaat tataactggg caagcatgga tgacatatta atatttgtca 400  
 gaattaagtg actcaaagtg ctatcgagag gtttttcaag tatctttgag 450  
 tttcatggcc aaagtgttaa ctagttttac tacaatgttt ggtgtttgtg 500  
 tggaaattat ctgcctggct t 521

<210> 305  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 305  
 ccaggaaatg ctccaggaag agcc 24

<210> 306  
 <211> 26  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 306  
 gcccatgaca ccaaattgaa gagtgg 26

<210> 307





acatcctctt ctgcacatac agaaaactcc agcagattgt cctgtaatcg 1100  
ctattgacag ctttaggcat atgtatgtgt ttggagactt caaagatgta 1150  
ttaattcctg gaaaactcaa gcaattcgta ttgacttac attctggaaa 1200  
actgcacaga gaattccatc atggacctga cccaactgat acagccccag 1250  
gagagcaagc ccaagatgta gcaagcagtc cacctgagag ctccttccag 1300  
aaactagcac ccagtgaata taggtatact ctattgaggg atcgagatga 1350  
gctttaaaaa cttgaaaaac agtttgtaag cctttcaaca gcagcatcaa 1400  
cctacgtggg ggaaatagta aacctatatt ttcataattc tatgtgtatt 1450  
tttattttga ataaacagaa agaaatttaa aaaaaaaaaa aaaaaaaaaa 1500  
aaaaaaaaaa aaaaaaaaaa aaa 1523

<210> 309  
<211> 406  
<212> PRT  
<213> Homo sapiens

<400> 309  
Met His Pro Ala Val Phe Leu Ser Leu Pro Asp Leu Arg Cys Ser  
1 5 10 15  
Leu Leu Leu Leu Val Thr Trp Val Phe Thr Pro Val Thr Thr Glu  
20 25 30  
Ile Thr Ser Leu Ala Thr Glu Asn Ile Asp Glu Ile Leu Asn Asn  
35 40 45  
Ala Asp Val Ala Leu Val Asn Phe Tyr Ala Asp Trp Cys Arg Phe  
50 55 60  
Ser Gln Met Leu His Pro Ile Phe Glu Glu Ala Ser Asp Val Ile  
65 70 75  
Lys Glu Glu Phe Pro Asn Glu Asn Gln Val Val Phe Ala Arg Val  
80 85 90  
Asp Cys Asp Gln His Ser Asp Ile Ala Gln Arg Tyr Arg Ile Ser  
95 100 105  
Lys Tyr Pro Thr Leu Lys Leu Phe Arg Asn Gly Met Met Met Lys  
110 115 120  
Arg Glu Tyr Arg Gly Gln Arg Ser Val Lys Ala Leu Ala Asp Tyr  
125 130 135  
Ile Arg Gln Gln Lys Ser Asp Pro Ile Gln Glu Ile Arg Asp Leu  
140 145 150  
Ala Glu Ile Thr Thr Leu Asp Arg Ser Lys Arg Asn Ile Ile Gly  
155 160 165



<222> 36, 48  
<223> unknown base

<400> 310  
attaaggaag aatttcctaaa tgaaaatcaa gtagtntttg ccagagtnga 50  
ttgtgatcag cactctgaca tagcccagag atacaggata agcaaatacc 100  
caaccctcaa attgtttcgt aatgggatga tgatgaagag agaatacagg 150  
ggtcagcgat cagtgaagc attggcagat ta 182

<210> 311  
<211> 598  
<212> DNA  
<213> Homo sapiens

<220>  
<221> unsure  
<222> 38, 59, 140, 169, 174, 183, 282-283, 294-295, 319, 396  
<223> unknown base

<400> 311  
agaggcctct ctggaagttg tcccgggtgt tcgccgcngg agcccgggtc 50  
gagaggacna ggtgccgctg cctggagaat cctccgctgc cgtcggctcc 100  
cggagcccag ccctttccta acccaaccca acctagcccn gtcccagccg 150  
ccagcgcttg tccctgtcnc gganccagc gtnaccatgc atcctgccgt 200  
cttcctatcc ttaccgcacc tcagatgctc cttctgtctc ctggtaactt 250  
gggtttttac tcctgtaaca actgaaataa cnngtcttga tacnnagaat 300  
atagatgaaa ttttaaacna tgctgatgtg gcttttagtca atttttatgc 350  
tgactggtgt cgtttcagtc agatgtggca tccaattttt gaggangctt 400  
ccgatgtcat taaggaagaa tttccaaatg aaaatcaagt agtgtttgcc 450  
agagttgatt gtgatcagca ctctgacata gccagagat acaggataag 500  
caaataccca accctcaaatt tgtttcgtaa tgggatgatg atgaagagag 550  
aatacagggg tcagcgatca gtgaaagcat tggcagatta catcaggc 598

<210> 312  
<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 312  
tgagaggcct ctctggaagt tg 22

```

<210> 313
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 313
    gtcagcgatc agtgaaagc 19

<210> 314
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 314
    ccagaatgaa gtagctcggc 20

<210> 315
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 315
    ccgactcaaa atgcattgtc 20

<210> 316
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 316
    catttggcag gaattgtcc 19

<210> 317
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 317
    ggtgctatag gccaaagg 18

<210> 318
<211> 24
<212> DNA

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 ttttgcttgt ggaaagactg ttttcatatg ttatactcag ataaagattt 650  
 taaatgggtat tacgtataaa ttaatatata atgattacct ctgggtgttga 700  
 cagggttgaa cttgcacttc ttaaggaaca gccataatcc tctgaatgat 750  
 gcattaatta ctgactgtcc tagtacattg gaagcttttg tttataggaa 800  
 cttgtagggc tcatttttgg ttcattgaaa cagtatctaa ttataaatta 850  
 gctgtagata tcagggtgct ctgatgaagt gaaaatgtat atctgactag 900  
 tgggaaactt catgggtttc ctcatctgtc atgtcgatga ttatatatgg 950  
 atacattttac aaaaataaaa agcgggaatt ttcccttcgc ttgaatatta 1000  
 tccctgtata ttgcatgaat gagagatttc ccatatttcc atcagagtaa 1050  
 taaatatact tgctttaatt ctttaagcata agtaaactg atataaaaaat 1100  
 atatgctgaa ttacttgtga agaattgcatt taaagctatt ttaaattgtgt 1150  
 ttttatttgt aagacattac ttattaagaa attgggttatt atgcttactg 1200  
 ttctaattctg gtggtaaagg tattcttaag aatttgcagg tactacagat 1250  
 tttcaaaact gaatgagaga aaattgtata accatcctgc tgttccttta 1300  
 gtgcaataca ataaaactct gaaattaaga ctc 1333

<210> 322  
 <211> 144  
 <212> PRT  
 <213> Homo sapiens

<400> 322  
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 1 5 10 15  
 Leu Thr Ala Ala Leu Ile Phe Phe Ala Ile Trp His Ile Ile Ala  
 20 25 30  
 Phe Asp Glu Leu Lys Thr Asp Tyr Lys Asn Pro Ile Asp Gln Cys  
 35 40 45  
 Asn Thr Leu Asn Pro Leu Val Leu Pro Glu Tyr Leu Ile His Ala  
 50 55 60  
 Phe Phe Cys Val Met Phe Leu Cys Ala Ala Glu Trp Leu Thr Leu  
 65 70 75  
 Gly Leu Asn Met Pro Leu Leu Ala Tyr His Ile Trp Arg Tyr Met  
 80 85 90  
 Ser Arg Pro Val Met Ser Gly Pro Gly Leu Tyr Asp Pro Thr Thr  
 95 100 105



<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 326  
gtgcagcaga gtggcttaca 20

<210> 327  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 327  
actggaccaa ttcttctgtg 20

<210> 328  
<211> 45  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 328  
gatattctag catattgtca gaaggaagga tgggtcaaatt tagct 45

<210> 329  
<211> 1174  
<212> DNA  
<213> Homo sapiens

<400> 329  
cggacgcgtg ggggaaaccc ttccgagaaa acagcaacaa gctgagctgc 50  
tgtgacagag gggaacaaga tggcggcgcc gaaggggagc ctctgggtga 100  
ggaccaact ggggctcccg ccgctgctgc tgctgaccat ggccttgcc 150  
ggaggttcgg ggaccgcttc ggctgaagca tttgactcgg tcttgggtga 200  
tacggcgtct tgccaccggg cctgtcagtt gacctacccc ttgcacacct 250  
accctaagga agaggagttg tacgcatgtc agagagggtg caggctgttt 300  
tcaatttgtc agtttgtgga tgatggaatt gacttaaata gaactaaatt 350  
ggaatgtgaa tctgcatgta cagaagcata ttcccaatct gatgagcaat 400  
atgcttgcca tcttggttgc cagaatcagc tgccattcgc tgaactgaga 450  
caagaacaac ttatgtccct gatgcaaaa atgcacctac tctttcctct 500



aactctggtg aggtcattct ggagtacat gatggactcc gcacagagct 550  
tcataacctc ttcattggact ttttatcttc aagccgatga cggaaaaata 600  
gttatattcc agtctaagcc agaaatccag tacgcaccac atttggagca 650  
ggagcctaca aatttgagag aatcatctct aagcaaaatg tcctatctgc 700  
aaatgagaaa ttcacaagcg cacaggaatt ttcttgaaga tggagaaagt 750  
gatggctttt taagatgcct ctctcttaac tctgggtgga ttttaactac 800  
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ttgctacagc tgtggagcag tatgttcctt ctgagaagct gagtatctat 900  
gggtgacttg agtttatgaa tgaacaaaag ctaaacagat atccagcttc 950  
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ctctacctac aaaagtgaat cttgctcatt ctgaaattta agcatttttc 1050  
ttttaaaaga caagtgtaat agacatctaa aattccactc ctcatagagc 1100  
ttttaaaatg gtttcattgg atataggcct taagaaatca ctataaaatg 1150  
caaataaagt tactcaaatc tgtg 1174

<210> 330  
<211> 323  
<212> PRT  
<213> Homo sapiens

<400> 330  
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Leu Pro Pro Leu Leu Leu Leu Thr Met Ala Leu Ala Gly Gly Ser  
20 25 30  
Gly Thr Ala Ser Ala Glu Ala Phe Asp Ser Val Leu Gly Asp Thr  
35 40 45  
Ala Ser Cys His Arg Ala Cys Gln Leu Thr Tyr Pro Leu His Thr  
50 55 60  
Tyr Pro Lys Glu Glu Glu Leu Tyr Ala Cys Gln Arg Gly Cys Arg  
65 70 75  
Leu Phe Ser Ile Cys Gln Phe Val Asp Asp Gly Ile Asp Leu Asn  
80 85 90  
Arg Thr Lys Leu Glu Cys Glu Ser Ala Cys Thr Glu Ala Tyr Ser  
95 100 105  
Gln Ser Asp Glu Gln Tyr Ala Cys His Leu Gly Cys Gln Asn Gln  
110 115 120

Leu	Pro	Phe	Ala	Glu	Leu	Arg	Gln	Glu	Gln	Leu	Met	Ser	Leu	Met	
				125					130					135	
Pro	Lys	Met	His	Leu	Leu	Phe	Pro	Leu	Thr	Leu	Val	Arg	Ser	Phe	
				140					145					150	
Trp	Ser	Asp	Met	Met	Asp	Ser	Ala	Gln	Ser	Phe	Ile	Thr	Ser	Ser	
				155					160					165	
Trp	Thr	Phe	Tyr	Leu	Gln	Ala	Asp	Asp	Gly	Lys	Ile	Val	Ile	Phe	
				170					175					180	
Gln	Ser	Lys	Pro	Glu	Ile	Gln	Tyr	Ala	Pro	His	Leu	Glu	Gln	Glu	
				185					190					195	
Pro	Thr	Asn	Leu	Arg	Glu	Ser	Ser	Leu	Ser	Lys	Met	Ser	Tyr	Leu	
				200					205					210	
Gln	Met	Arg	Asn	Ser	Gln	Ala	His	Arg	Asn	Phe	Leu	Glu	Asp	Gly	
				215					220					225	
Glu	Ser	Asp	Gly	Phe	Leu	Arg	Cys	Leu	Ser	Leu	Asn	Ser	Gly	Trp	
				230					235					240	
Ile	Leu	Thr	Thr	Thr	Leu	Val	Leu	Ser	Val	Met	Val	Leu	Leu	Trp	
				245					250					255	
Ile	Cys	Cys	Ala	Thr	Val	Ala	Thr	Ala	Val	Glu	Gln	Tyr	Val	Pro	
				260					265					270	
Ser	Glu	Lys	Leu	Ser	Ile	Tyr	Gly	Asp	Leu	Glu	Phe	Met	Asn	Glu	
				275					280					285	
Gln	Lys	Leu	Asn	Arg	Tyr	Pro	Ala	Ser	Ser	Leu	Val	Val	Val	Arg	
				290					295					300	
Ser	Lys	Thr	Glu	Asp	His	Glu	Glu	Ala	Gly	Pro	Leu	Pro	Thr	Lys	
				305					310					315	
Val	Asn	Leu	Ala	His	Ser	Glu	Ile								
				320											

<210> 331  
 <211> 350  
 <212> DNA  
 <213> Homo sapiens

<400> 331  
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 gcacacctac cctaaggaag aggagttgta cgcattgtcag agaggttgca 100  
 ggctgttttc aatttgtcag tttgtggatg atggaattga cttaaattcga 150  
 actaaattgg aatgtgaatc tgcatgtaca gaagcatatt cccaattctga 200  
 tgagcaatat gcttgccatc ttggttgcca gaatcagctg ccattcgctg 250

aactgagaca agaacaactt atgtccctga tgccaaaaat gcacctactc 300  
 tttcctctaa ctctggtgag gtcattctgg agtgacatga tggactccgc 350

<210> 332  
 <211> 562  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> unsure  
 <222> 47  
 <223> unknown base

<400> 332  
 cacactggcc ggatctttta gaggcctttg accttgacca agggctcngga 50  
 aaacagcaac aagctgagct gctgtgacag agggaacaag atggcggcgc 100  
 cgaagggagc ctttggggtga ggaccaact ggggctcccg ccgctgctgc 150  
 tgctgaccat ggccttgagg ggaggttcgg ggaccgcttc ggctgaagca 200  
 tttgactcgg tcttggggtga tacggcgtct tgccaccggg cctgtcagtt 250  
 gacctacccc ttgcacacct accctaagga agaggagttg tacgcatgtc 300  
 agagaggttg caggctgttt tcaatttgtc agtttgtgga tgatggaatt 350  
 gacttaaata gaactaaatt ggaatgtgaa tctgcatgta cagaagcata 400  
 ttcccaatct gatgagcaat atgcttgcca tcttggttgc cagaatcagc 450  
 tgccattcgc tgaactgaga caagaacaac ttatgtccct gatgccaaaa 500  
 atgcacctac tctttcctct aactctggtg aggtcattct ggagtgcacat 550  
 gatggactcc gc 562

<210> 333  
 <211> 22  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 333  
 acaagctgag ctgctgtgac ag 22

<210> 334  
 <211> 22  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 334  
tgattctggc aaccaagatg gc 22

<210> 335

<211> 40

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 335

atggccttgg ccggagggtc ggggaccgct tcggctgaag 40

<210> 336

<211> 1885

<212> DNA

<213> Homo sapiens

<400> 336

gcgagggtggc gatcgctgag aggcaggagg gccgaggcgg gcctgggagg 50  
cggcccggag gtggggcgcc gctggggccg gcccgcacgg gcttcatctg 100  
agggcgcacg gcccgcgacc gagcgtgcgg actggcctcc caagcgtggg 150  
gcgacaagct gccggagctg caatggggccg cggctgggga ttcttgtttg 200  
gcctcctggg cgccgtgttg ctgctcagct cgggccacgg agaggagcag 250  
cccccggaga cagcggcaca gaggtgcttc tgccagggtta gtggttactt 300  
ggatgattgt acctgtgatg ttgaaaccat tgatagattt aataactaca 350  
ggcttttccc aagactacaa aaacttcttg aaagtgacta ctttaggtat 400  
tacaaggtaa acctgaagag gccgtgtcct ttctggaatg acatcagcca 450  
gtgtggaaga agggactgtg ctgtcaaacc atgtcaatct gatgaagtgc 500  
ctgatggaat taaatctgag agctacaagt attctgaaga agccaataat 550  
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tctgagttag gaaacacaga aggtgtttct tcagtggacc aagcatgatg 650  
attcttcaga taacttctgt gaagctgatg acattcagtc ccctgaagct 700  
gaatatgtag atttgcttct taatcctgag cgctacactg gttacaaggg 750  
accagatgct tggaaaatat ggaatgtcat ctacgaagaa aactgtttta 800  
agccacagac aattaaaaga cttttaaatc ctttggcttc tggatcaagg 850  
acaagtgaag agaacacttt ttacagttgg ctagaaggtc tctgtgtaga 900  
aaaaagagca ttctacagac ttatatctgg cctacatgca agcattaatg 950

tgcatttgag tgcaagatat cttttacaag agacctgggtt agaaaagaaa 1000  
 tggggacaca acattacaga atttcaacag cgatttgatg gaattttgac 1050  
 tgaaggagaa ggtccaagaa ggcttaagaa cttgtatttt ctctacttaa 1100  
 tagaactaag ggctttatcc aaagtgttac cattcttcga gcgcccagat 1150  
 tttcaactct ttactggaaa taaaattcag gatgaggaaa acaaaatggt 1200  
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 agaattcatt ttttgctggg gataaaaaag aagcacacaa actaaaggag 1300  
 gactttcgac tgcattttag aaatatttca agaattatgg attgtgttgg 1350  
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 ctgctctgaa gatcttattt tctgagaaat tgatagcaaa tatgccagaa 1450  
 agtggacctt gttatgaatt ccatctaacc agacaagaaa tagtatcatt 1500  
 attcaacgca tttggaagaa tttctacaag tgtgaaagaa ttagaaaact 1550  
 tcaggaactt gttacagaat attcattaaa gaaaacaagc tgatatgtgc 1600  
 ctgtttctgg acaatggagg cgaaagagtg gaatttcatt caaaggcata 1650  
 atagcaatga cagtcttaag ccaaacattt tatataaagt tgcttttgta 1700  
 aaggagaatt atattgtttt aagtaaacac atttttaaaa attgtgttaa 1750  
 gtctatgtat aatactactg tgagtaaaag taatacttta ataatgtggt 1800  
 acaaatttta aagttaata ttgaataaaa ggaggattat caaattaaaa 1850  
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaa 1885

<210> 337

<211> 468

<212> PRT

<213> Homo sapiens

<400> 337

Met	Gly	Arg	Gly	Trp	Gly	Phe	Leu	Phe	Gly	Leu	Leu	Gly	Ala	Val
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Trp	Leu	Leu	Ser	Ser	Gly	His	Gly	Glu	Glu	Gln	Pro	Pro	Glu	Thr
			20					25						30
Ala	Ala	Gln	Arg	Cys	Phe	Cys	Gln	Val	Ser	Gly	Tyr	Leu	Asp	Asp
			35						40					45
Cys	Thr	Cys	Asp	Val	Glu	Thr	Ile	Asp	Arg	Phe	Asn	Asn	Tyr	Arg
			50					55						60
Leu	Phe	Pro	Arg	Leu	Gln	Lys	Leu	Leu	Glu	Ser	Asp	Tyr	Phe	Arg
			65					70						75

Tyr	Tyr	Lys	Val	Asn	Leu	Lys	Arg	Pro	Cys	Pro	Phe	Trp	Asn	Asp		80	85	90
Ile	Ser	Gln	Cys	Gly	Arg	Arg	Asp	Cys	Ala	Val	Lys	Pro	Cys	Gln		95	100	105
Ser	Asp	Glu	Val	Pro	Asp	Gly	Ile	Lys	Ser	Ala	Ser	Tyr	Lys	Tyr		110	115	120
Ser	Glu	Glu	Ala	Asn	Asn	Leu	Ile	Glu	Glu	Cys	Glu	Gln	Ala	Glu		125	130	135
Arg	Leu	Gly	Ala	Val	Asp	Glu	Ser	Leu	Ser	Glu	Glu	Thr	Gln	Lys		140	145	150
Ala	Val	Leu	Gln	Trp	Thr	Lys	His	Asp	Asp	Ser	Ser	Asp	Asn	Phe		155	160	165
Cys	Glu	Ala	Asp	Asp	Ile	Gln	Ser	Pro	Glu	Ala	Glu	Tyr	Val	Asp		170	175	180
Leu	Leu	Leu	Asn	Pro	Glu	Arg	Tyr	Thr	Gly	Tyr	Lys	Gly	Pro	Asp		185	190	195
Ala	Trp	Lys	Ile	Trp	Asn	Val	Ile	Tyr	Glu	Glu	Asn	Cys	Phe	Lys		200	205	210
Pro	Gln	Thr	Ile	Lys	Arg	Pro	Leu	Asn	Pro	Leu	Ala	Ser	Gly	Gln		215	220	225
Gly	Thr	Ser	Glu	Glu	Asn	Thr	Phe	Tyr	Ser	Trp	Leu	Glu	Gly	Leu		230	235	240
Cys	Val	Glu	Lys	Arg	Ala	Phe	Tyr	Arg	Leu	Ile	Ser	Gly	Leu	His		245	250	255
Ala	Ser	Ile	Asn	Val	His	Leu	Ser	Ala	Arg	Tyr	Leu	Leu	Gln	Glu		260	265	270
Thr	Trp	Leu	Glu	Lys	Lys	Trp	Gly	His	Asn	Ile	Thr	Glu	Phe	Gln		275	280	285
Gln	Arg	Phe	Asp	Gly	Ile	Leu	Thr	Glu	Gly	Glu	Gly	Pro	Arg	Arg		290	295	300
Leu	Lys	Asn	Leu	Tyr	Phe	Leu	Tyr	Leu	Ile	Glu	Leu	Arg	Ala	Leu		305	310	315
Ser	Lys	Val	Leu	Pro	Phe	Phe	Glu	Arg	Pro	Asp	Phe	Gln	Leu	Phe		320	325	330
Thr	Gly	Asn	Lys	Ile	Gln	Asp	Glu	Glu	Asn	Lys	Met	Leu	Leu	Leu		335	340	345
Glu	Ile	Leu	His	Glu	Ile	Lys	Ser	Phe	Pro	Leu	His	Phe	Asp	Glu		350	355	360
Asn	Ser	Phe	Phe	Ala	Gly	Asp	Lys	Lys	Glu	Ala	His	Lys	Leu	Lys				

365	370	375
Glu Asp Phe Arg Leu His Phe Arg Asn Ile Ser Arg Ile Met Asp		
380	385	390
Cys Val Gly Cys Phe Lys Cys Arg Leu Trp Gly Lys Leu Gln Thr		
395	400	405
Gln Gly Leu Gly Thr Ala Leu Lys Ile Leu Phe Ser Glu Lys Leu		
410	415	420
Ile Ala Asn Met Pro Glu Ser Gly Pro Ser Tyr Glu Phe His Leu		
425	430	435
Thr Arg Gln Glu Ile Val Ser Leu Phe Asn Ala Phe Gly Arg Ile		
440	445	450
Ser Thr Ser Val Lys Glu Leu Glu Asn Phe Arg Asn Leu Leu Gln		
455	460	465
Asn Ile His		

<210> 338  
 <211> 507  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> unsure  
 <222> 101, 263, 376, 397, 426  
 <223> unknown base

<400> 338  
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 nacacttttt acagttggct agaaggtctc tgtgtagaaa aaagagcatt 150  
 ctacagactt atatctggcc tacatgcaag cattaatgtg cttttgagtg 200  
 caagatatct ttacaagag acctgggttag aaaagaaatg gggacacaac 250  
 attacagaat ttnaacagcg atttgatgga attttgactg aaggagaagg 300  
 tccaagaagg cttaagaact tgtattttct ctacttaata gaactaaggg 350  
 ctttatccaa agtgttacca ttcttngagc gccagattt tcaactnttt 400  
 actggaaata aaattcagga tgaggnaaac aaaatgttac ttttggaat 450  
 acttcatgaa atcaagtcatt ttcctttgca ttttgatgag aattcatttt 500  
 tttgctg 507

<210> 339  
 <211> 20

<212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic oligonucleotide probe  
  
 <400> 339  
 aagctgccgg agctgcaatg 20  
  
 <210> 340  
 <211> 21  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic oligonucleotide probe  
  
 <400> 340  
 ttgcttctta atcctgagcg c 21  
  
 <210> 341  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic oligonucleotide probe  
  
 <400> 341  
 aaaggaggac tttcgactgc 20  
  
 <210> 342  
 <211> 26  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic oligonucleotide probe  
  
 <400> 342  
 agagattcat ccactgctcc aagtcg 26  
  
 <210> 343  
 <211> 25  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic oligonucleotide probe  
  
 <400> 343  
 tgtccagaaa caggcacata tcagc 25  
  
 <210> 344  
 <211> 50  
 <212> DNA  
 <213> Artificial Sequence



<220>  
<223> Synthetic oligonucleotide probe

<400> 344  
agacagcggc acagaggtgc ttctgccagg ttagtgggta cttggatgat 50

<210> 345  
<211> 1486  
<212> DNA  
<213> Homo sapiens

<400> 345  
cggacgcgtg ggcggacgcg tgggcggacg cgtgggttgg gagggggcag 50  
gatgggaggg aaagtgaaga aaacagaaaa ggagagggac agaggccaga 100  
ggactttctca tactggacag aaaccgatca ggcatggaac tccccttcgt 150  
cactcacctg ttcttgcccc tgggtttcct gacaggtctc tgctccccct 200  
ttaacctgga tgaacatcac ccacgcctat tcccagggcc accagaagct 250  
gaatttggat acagtgtctt acaacatgtt ggggggtggac agcgatggat 300  
gctggtgggc gccccctggg atgggccttc aggcgaccgg aggggggacg 350  
tttatcgctg ccctgtaggg gggggccaca atgccccatg tgccaagggc 400  
cacttaggtg actaccaact gggaaattca tctcatcctg ctgtgaatat 450  
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aaagagaagt gtggttaagg aaaatggtct gtgtggaggg gtcaaggagt 600  
taaaaaccct agaaagcaaa aggtaggtaa tgtcaggag tagtcttcat 650  
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attccagcct cagggaagcc tggcaccac tgcccaacgt gagccagagg 850  
aaggctgagt acttggttcc cagaaggaga tactgggtgg gaaaaagatg 900  
gggcaaagcg gtatgatgcc tggcaaaggg cctgcatggc tatcctcatt 950  
gctaccta atgtgcttcaa aagctccatg tttcctaaca gattcagact 1000  
cctggccagg tgtggtggcc cacacctgta attctagcac tttgggaggc 1050  
caagggtggc agatcacttg aggtcaggag ttcaagacca gcctggccaa 1100  
catggtgaaa ctccatctct actaaaaaaa aaaaaataca aaaattagct 1150

ggggtgcgcta gtgcatgcct gtaatctcat ctactcggga ggctaagaca 1200  
 ggagactctc acttcaaccc aggaggtgga ggttgcggtg agccaagatt 1250  
 gtgcctctgc actctagcgt gggtgacaga gtaagcgaga ctccatctca 1300  
 aaaataataa taataataat tcagactcct tatcaggagt ccatgatctg 1350  
 gcctggcaca gtaactcatg cctgtaatcc caacattttg ggaggccaac 1400  
 gcaggaggat tgcttgaggt ctggagggtt gagaccagcc tgggcaacat 1450  
 agaagagccc catctctaaa taaatgtttt aaaaat 1486

<210> 346  
 <211> 124  
 <212> PRT  
 <213> Homo sapiens

<400> 346  
 Met Glu Leu Pro Phe Val Thr His Leu Phe Leu Pro Leu Val Phe  
 1 5 10 15  
 Leu Thr Gly Leu Cys Ser Pro Phe Asn Leu Asp Glu His His Pro  
 20 25 30  
 Arg Leu Phe Pro Gly Pro Pro Glu Ala Glu Phe Gly Tyr Ser Val  
 35 40 45  
 Leu Gln His Val Gly Gly Gly Gln Arg Trp Met Leu Val Gly Ala  
 50 55 60  
 Pro Trp Asp Gly Pro Ser Gly Asp Arg Arg Gly Asp Val Tyr Arg  
 65 70 75  
 Cys Pro Val Gly Gly Ala His Asn Ala Pro Cys Ala Lys Gly His  
 80 85 90  
 Leu Gly Asp Tyr Gln Leu Gly Asn Ser Ser His Pro Ala Val Asn  
 95 100 105  
 Met His Leu Gly Met Ser Leu Leu Glu Thr Asp Gly Asp Gly Gly  
 110 115 120  
 Phe Met Val Ser

<210> 347  
 <211> 509  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> unsure  
 <222> 22  
 <223> unknown base

<400> 347



<213> Homo sapiens

<400> 351

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catctggggt tgggcagaaa ggaggggtgct tcggagcccg ccctttctga 100  
gcttcctggg ccggctctag aacaattcag gcttcgctgc gactcagacc 150  
tcagctccaa catatgcatt ctgaagaaa atggctgaga tggacagaat 200  
gctttatattt ggaaagaaac aatgttctag gtcaaactga gtctacaaa 250  
tgcagacttt cacaatgggt ctagaagaaa tctggacaag tcttttcatg 300  
tggtttttct acgcattgat tccatgtttg ctcacagatg aagtggccat 350  
tctgcctgcc cctcagaacc tctctgtact ctcaaccaac atgaagcatc 400  
tcttgatgtg gagcccagtg atcgcgcctg gagaaacagt gtactattct 450  
gtcgaatacc agggggagta cgagagcctg tacacgagcc acatctggat 500  
ccccagcagc tgggtgtcac tcaactgaagg tcctgagtgt gatgtcactg 550  
atgacatcac ggccactgtg ccatacaacc ttcgtgtcag ggccacattg 600  
gggtcacaga cctcagcctg gagcatcctg aagcatccct ttaatagaaa 650  
ctcaaccatc cttacccgac ctgggatgga gatcacaaa gatggcttcc 700  
acctggttat tgagctggag gacctggggc ccagtttga gttccttgtg 750  
gcctactgga ggagggagcc tggtgccgag gaacatgtca aaatggtgag 800  
gagtgggggt attccagtgc acctagaaac catggagcca ggggctgcat 850  
actgtgtgaa ggcccagaca ttcgtgaagg ccattgggag gtacagcgcc 900  
ttcagccaga cagaatgtgt ggaggtgcaa ggagaggcca ttcccctggt 950  
actggccctg tttgcctttg ttggcttcat gctgacctt gtggtcgtgc 1000  
cactgttcgt ctggaaaatg ggccggctgc tccagtactc ctgttgcccc 1050  
gtggtggtcc tcccagacac cttgaaaata accaattcac ccagaagtt 1100  
aatcagctgc agaaggagg aggtggatgc ctgtgccacg gctgtgatgt 1150  
ctcctgagga actcctcagg gcctggatct cataggtttg cggaagggcc 1200  
caggtgaagc cgagaacctg gtctgcatga catggaaacc atgaggggac 1250  
aagttgtgtt tctgttttcc gccacggaca agggatgaga gaagtaggaa 1300  
gagcctgttg tctacaagtc tagaagcaac catcagaggc agggtggttt 1350  
gtctaacaga aactgactg aggetttaggg gatgtgacct ctagactggg 1400

ggctgccact tgctggctga gcaaccctgg gaaaagtac ttcacccctt 1450  
 cggtcctaag ttttctcatc tgtaatgggg gaattaccta cacacctgct 1500  
 aaacacacac acacagagtc tctctctata tatacacacg tacacataaa 1550  
 tacaccagc acttgcaagg ctagagggaa actggtgaca ctctacagtc 1600  
 tgactgattc agtgtttctg gagagcagga cataaatgta tgatgagaat 1650  
 gatcaaggac tctacacact ggggtggcttg gagagcccac tttcccagaa 1700  
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 gtgacctgga ggaaggtcac agccacactg aaaatgggat gtgcatgaac 1850  
 acggaggatc catgaactac tgtaaagtgt tgacagtgtg tgcacactgc 1900  
 agacagcagg tgaaatgtat gtgtgcaatg cgacgagaat gcagaagtca 1950  
 gtaacatgtg catgtttgtt gtgctccttt tttctgttgg taaagtacag 2000  
 aattcagcaa ataaaaaggg ccaccctggc caaaagcggg aaaaaaaaaa 2050  
 aaaaaa 2056

<210> 352  
 <211> 311  
 <212> PRT  
 <213> Homo sapiens

<400> 352  
 Met Gln Thr Phe Thr Met Val Leu Glu Glu Ile Trp Thr Ser Leu  
 1 5 10 15  
 Phe Met Trp Phe Phe Tyr Ala Leu Ile Pro Cys Leu Leu Thr Asp  
 20 25 30  
 Glu Val Ala Ile Leu Pro Ala Pro Gln Asn Leu Ser Val Leu Ser  
 35 40 45  
 Thr Asn Met Lys His Leu Leu Met Trp Ser Pro Val Ile Ala Pro  
 50 55 60  
 Gly Glu Thr Val Tyr Tyr Ser Val Glu Tyr Gln Gly Glu Tyr Glu  
 65 70 75  
 Ser Leu Tyr Thr Ser His Ile Trp Ile Pro Ser Ser Trp Cys Ser  
 80 85 90  
 Leu Thr Glu Gly Pro Glu Cys Asp Val Thr Asp Asp Ile Thr Ala  
 95 100 105  
 Thr Val Pro Tyr Asn Leu Arg Val Arg Ala Thr Leu Gly Ser Gln  
 110 115 120

Thr	Ser	Ala	Trp	Ser	Ile	Leu	Lys	His	Pro	Phe	Asn	Arg	Asn	Ser	
				125					130					135	
Thr	Ile	Leu	Thr	Arg	Pro	Gly	Met	Glu	Ile	Thr	Lys	Asp	Gly	Phe	
				140					145					150	
His	Leu	Val	Ile	Glu	Leu	Glu	Asp	Leu	Gly	Pro	Gln	Phe	Glu	Phe	
				155					160					165	
Leu	Val	Ala	Tyr	Trp	Arg	Arg	Glu	Pro	Gly	Ala	Glu	Glu	His	Val	
				170					175					180	
Lys	Met	Val	Arg	Ser	Gly	Gly	Ile	Pro	Val	His	Leu	Glu	Thr	Met	
				185					190					195	
Glu	Pro	Gly	Ala	Ala	Tyr	Cys	Val	Lys	Ala	Gln	Thr	Phe	Val	Lys	
				200					205					210	
Ala	Ile	Gly	Arg	Tyr	Ser	Ala	Phe	Ser	Gln	Thr	Glu	Cys	Val	Glu	
				215					220					225	
Val	Gln	Gly	Glu	Ala	Ile	Pro	Leu	Val	Leu	Ala	Leu	Phe	Ala	Phe	
				230					235					240	
Val	Gly	Phe	Met	Leu	Ile	Leu	Val	Val	Val	Pro	Leu	Phe	Val	Trp	
				245					250					255	
Lys	Met	Gly	Arg	Leu	Leu	Gln	Tyr	Ser	Cys	Cys	Pro	Val	Val	Val	
				260					265					270	
Leu	Pro	Asp	Thr	Leu	Lys	Ile	Thr	Asn	Ser	Pro	Gln	Lys	Leu	Ile	
				275					280					285	
Ser	Cys	Arg	Arg	Glu	Glu	Val	Asp	Ala	Cys	Ala	Thr	Ala	Val	Met	
				290					295					300	
Ser	Pro	Glu	Glu	Leu	Leu	Arg	Ala	Trp	Ile	Ser					
				305					310						

<210> 353  
 <211> 864  
 <212> DNA  
 <213> Homo sapiens  
  
 <220>  
 <221> unsure  
 <222> 654, 711, 748, 827  
 <223> unknown base

<400> 353  
 tcctgctgat gcacatctgg gtttggcaaa aggaggttgc ttcgagccgc 50  
 cctttctagc ttcctggccg gctctagaac aattcaggct tcgctgcgac 100  
 tagacctcag ctccaacata tgcattctga agaaagatgg ctgagatgac 150  
 agaatgcttt attttggaaa gaaacaatgt tctaggtcaa actgagtcta 200

ccaaatgcag actttcaciaa tggttctaga agaaatctgg acaagtcttt 250  
 tcatgtgggtt tttctacgca ttgattccat gtttgctcac agatgaagtg 300  
 gccattctgc ctgcccctca gaacctctct gtactctcaa ccaacatgaa 350  
 gcatctcttg atgtggagcc cagtgatcgc gcctggagaa acagtgtact 400  
 attctgtcga ataccagggg gagtacgaga gcctgtacac gagccacatc 450  
 tggatcccca gcagctggtg ctactcact gaaggtcctg agtgtgatgt 500  
 cactgatgac atcacggcca ctgtgccata caacctttgt gtcagggcca 550  
 cattgggctc acagacctca gcctggagca tcctgaagca tccctttaat 600  
 agaaactcaa ccataccttac ccgacctggg atggagatca ccaaagatgg 650  
 cttncacctg gttattgagc tggaggacct ggggccccag tttgagttcc 700  
 ttgtggccta ntggaggagg ggcgaacccc ttgcggcgca aggggttngc 750  
 gaaccccttg cggccgctgg ggtatctctc gagaaaagag aggcccaata 800  
 tgaccacat actcaatatg gacgaantgc tattgtccac ctgtttgagt 850  
 ggcgctgggt tgat 864

- <210> 354
- <211> 23
- <212> DNA
- <213> Artificial Sequence
- <220>
- <223> Synthetic oligonucleotide probe
- <400> 354
- aggcttcgct gcgactagac ctc 23
- <210> 355
- <211> 24
- <212> DNA
- <213> Artificial Sequence
- <220>
- <223> Synthetic oligonucleotide probe
- <400> 355
- ccaggtcggg taaggatggt tgag 24
- <210> 356
- <211> 50
- <212> DNA
- <213> Artificial Sequence
- <220>
- <223> Synthetic oligonucleotide probe





gagcctggag ctctgttcc ctgaatcctt cggcttcac acctatcagg 1300  
gctctctcag caccgccccc tgctccgaga ctgtcacctg gatcctcatt 1350  
gaccggggccc tcaatatcac ctcccttcag atgcactccc tgagactcct 1400  
gagccagaat cctccatctc agatcttcca gagcctcagc ggtaacagcc 1450  
ggcccctgca gcccttggcc cacagggcac tgaggggcaa cagggacccc 1500  
cggcaccgcc agaggcgctg ccgaggcccc aactaccgcc tgcattgtga 1550  
tggtgtcccc catggtcgct gagactcccc ttcgaggatt gcaccgcc 1600  
gtcctaagcc tccccacaag gcgaggggag ttaccctaa aacaaagcta 1650  
ttaaagggac agaatactta 1670

<210> 358  
<211> 328  
<212> PRT  
<213> Homo sapiens

<400> 358  
Met Gly Ala Ala Ala Arg Leu Ser Ala Pro Arg Ala Leu Val Leu  
1 5 10 15  
Trp Ala Ala Leu Gly Ala Ala Ala His Ile Gly Pro Ala Pro Asp  
20 25 30  
Pro Glu Asp Trp Trp Ser Tyr Lys Asp Asn Leu Gln Gly Asn Phe  
35 40 45  
Val Pro Gly Pro Pro Phe Trp Gly Leu Val Asn Ala Ala Trp Ser  
50 55 60  
Leu Cys Ala Val Gly Lys Arg Gln Ser Pro Val Asp Val Glu Leu  
65 70 75  
Lys Arg Val Leu Tyr Asp Pro Phe Leu Pro Pro Leu Arg Leu Ser  
80 85 90  
Thr Gly Gly Glu Lys Leu Arg Gly Thr Leu Tyr Asn Thr Gly Arg  
95 100 105  
His Val Ser Phe Leu Pro Ala Pro Arg Pro Val Val Asn Val Ser  
110 115 120  
Gly Gly Pro Leu Leu Tyr Ser His Arg Leu Ser Glu Leu Arg Leu  
125 130 135  
Leu Phe Gly Ala Arg Asp Gly Ala Gly Ser Glu His Gln Ile Asn  
140 145 150  
His Gln Gly Phe Ser Ala Glu Val Gln Leu Ile His Phe Asn Gln  
155 160 165  
Glu Leu Tyr Gly Asn Phe Ser Ala Ala Ser Arg Gly Pro Asn Gly

	170		175		180
Leu Ala Ile Leu Ser Leu Phe Val Asn Val Ala Ser Thr Ser Asn					
	185		190		195
Pro Phe Leu Ser Arg Leu Leu Asn Arg Asp Thr Ile Thr Arg Ile					
	200		205		210
Ser Tyr Lys Asn Asp Ala Tyr Phe Leu Gln Asp Leu Ser Leu Glu					
	215		220		225
Leu Leu Phe Pro Glu Ser Phe Gly Phe Ile Thr Tyr Gln Gly Ser					
	230		235		240
Leu Ser Thr Pro Pro Cys Ser Glu Thr Val Thr Trp Ile Leu Ile					
	245		250		255
Asp Arg Ala Leu Asn Ile Thr Ser Leu Gln Met His Ser Leu Arg					
	260		265		270
Leu Leu Ser Gln Asn Pro Pro Ser Gln Ile Phe Gln Ser Leu Ser					
	275		280		285
Gly Asn Ser Arg Pro Leu Gln Pro Leu Ala His Arg Ala Leu Arg					
	290		295		300
Gly Asn Arg Asp Pro Arg His Pro Glu Arg Arg Cys Arg Gly Pro					
	305		310		315
Asn Tyr Arg Leu His Val Asp Gly Val Pro His Gly Arg					
	320		325		

<210> 359

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 359

tctgctgagg tgcagctcat tcac 24

<210> 360

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 360

gaggctctgg aagatctgag atgg 24

<210> 361

<211> 50

<212> DNA

<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 361  
gcctctttgt caacgttgcc agtacctcta acccattcct cagtcgcctc 50

<210> 362  
<211> 3038  
<212> DNA  
<213> Homo sapiens

<400> 362  
ggcgcctggt tctgcgcgta ctggctgtac ggagcaggag caagaggtcg 50  
ccgccagcct ccgccgccga gcctcggttcg tgtccccgcc cctcgctcct 100  
gcagctactg ctacagaaacg ctggggcgcc caccctggca gactaacgaa 150  
gcagctccct tcccacccca actgcaggtc taattttgga cgctttgcct 200  
gccatttctt ccaggttgag ggagccgcag aggcggaggc tcgcgtattc 250  
ctgcagtcag caccacagtc gcccccgac gctcgggtgct caggcccttc 300  
gcgagcgggg ctctccgtct gcggctccctt gtgaaggctc tgggcggctg 350  
cagaggccgg ccgtccggtt tggctcacct ctcccaggaa acttcacact 400  
ggagagccaa aaggagtgga agagcctgtc ttggagattt tcctggggaa 450  
atcctgaggt cattcattat gaagtgtacc gcgcgggagt ggctcagagt 500  
aaccacagtg ctgttcattg ctagagcaat tccagccatg gtggttccca 550  
atgccacttt attggagaaa cttttggaaa aatacatgga tgaggatggt 600  
gagtgggtgga tagccaaaca acgagggaaa agggccatca cagacaatga 650  
catgcagagt attttgacc ttcataataa attacgaagt cagggtgtatc 700  
caacagcctc taatatggag tatatgacat gggatgtaga gctggaaaga 750  
tctgcagaat cctgggctga aagttgcttg tgggaacatg gacctgcaag 800  
cttgcttcca tcaattggac agaatttggg agcacactgg ggaagatata 850  
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tggccctgta tgtacacatt atacacaggt cgtgtgggca actagtaaca 1000  
gaatcggttg tgccattaat ttgtgtcata acatgaacat ctgggggcag 1050  
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ctggtggggc catgcccctt acaaacatgg gcggccctgt tctgcttgcc 1150

cacctagttt tggagggggc tgtagagaaa atctgtgcta caaagaagg 1200  
tcagacaggt attatcccc tcgagaagag gaaacaaatg aaatagaacg 1250  
acagcagtca caagtccatg acacccatgt ccggacaaga tcagatgata 1300  
gtagcagaaa tgaagtcata agcgcacagc aaatgtccca aattgtttct 1350  
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cgaatgtcct gctggctgtt tggatagtaa agctaaagt attggcagt 1450  
tacattatga aatgcaatcc agcatctgta gagctgcaat tcattatggt 1500  
ataatagaca atgatggtgg ctgggtagat atcactagac aaggaagaaa 1550  
gcattatttc atcaagtcca atagaaatgg tattcaaaca attggcaa 1600  
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acttgtgaaa caactgtgga acagctctgt ccatttcata agcctgcttc 1700  
acattgcccc agagtatact gtcctcgtaa ctgtatgcaa gcaaatccac 1750  
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tgcagagcag cagtacatgc tggagtgggt cgaaatcacg gtggttatgt 1850  
tgatgtaatg cctgtggaca aaagaaagac ctacattgct tcttttcaga 1900  
atggaatctt ctcaaaaagt ttacagaatc ctccaggagg aaaggcattc 1950  
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taaactctga taaacaaaagt ctataaaata aaacatggga cattagcttt 2150  
gggaaaagta atgaaaatat aatggtttta gaaatcctgt gttaaattatt 2200  
gctatatttt cttagcagtt atttctacag ttaattacat agtcatgatt 2250  
gttctacgtt tcatatatta tatggtgctt tgtatatgcc actaataaaa 2300  
tgaatctaaa cattgaatgt gaatggccct cagaaaatca tctagtgc 2350  
ttaaaaataa tcgactctaa aactgaaaga aaccttatca cattttcccc 2400  
agttcaatgc tatgccatta ccaactccaa ataactctca ataattttcc 2450  
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aaattctgat attgcacttc ttattttata taaaataatc ctttaatatc 2550  
caaatgaatc tgtaaaaatg ttgattcct tgggaatggc cttaaaaata 2600

aatgtaataa agtcagagtg gtggtatgaa aacattccta gtgatcatgt 2650  
 agtaaagtga ggggttaagca tggacagcca gagctttcta tgtactgtta 2700  
 aaattgaggt cacatatattt cttttgtatc ctggcaaata ctcctgcagg 2750  
 ccaggaagta taatagcaaa aagttgaaca aagatgaact aatgtattac 2800  
 attaccattg ccaactgattt tttttaaatg gtaaatgacc ttgtatataa 2850  
 atattgccat atcatggtac ctataatggt gatatatattg tttctatgaa 2900  
 aaatgtattg tgctttgata ctaaaaatct gtaaaatggt agttttggtta 2950  
 attttttttc tgctggtgga tttacatatt aaattttttc tgctggtgga 3000  
 taaacattaa aattaatcat gtttcaaaaa aaaaaaaa 3038

<210> 363

<211> 500

<212> PRT

<213> Homo sapiens

<400> 363

Met Lys Cys Thr Ala Arg Glu Trp Leu Arg Val Thr Thr Val Leu  
 1 5 10 15

Phe Met Ala Arg Ala Ile Pro Ala Met Val Val Pro Asn Ala Thr  
 20 25 30

Leu Leu Glu Lys Leu Leu Glu Lys Tyr Met Asp Glu Asp Gly Glu  
 35 40 45

Trp Trp Ile Ala Lys Gln Arg Gly Lys Arg Ala Ile Thr Asp Asn  
 50 55 60

Asp Met Gln Ser Ile Leu Asp Leu His Asn Lys Leu Arg Ser Gln  
 65 70 75

Val Tyr Pro Thr Ala Ser Asn Met Glu Tyr Met Thr Trp Asp Val  
 80 85 90

Glu Leu Glu Arg Ser Ala Glu Ser Trp Ala Glu Ser Cys Leu Trp  
 95 100 105

Glu His Gly Pro Ala Ser Leu Leu Pro Ser Ile Gly Gln Asn Leu  
 110 115 120

Gly Ala His Trp Gly Arg Tyr Arg Pro Pro Thr Phe His Val Gln  
 125 130 135

Ser Trp Tyr Asp Glu Val Lys Asp Phe Ser Tyr Pro Tyr Glu His  
 140 145 150

Glu Cys Asn Pro Tyr Cys Pro Phe Arg Cys Ser Gly Pro Val Cys  
 155 160 165

Thr His Tyr Thr Gln Val Val Trp Ala Thr Ser Asn Arg Ile Gly

	170		175		180
Cys Ala Ile Asn	Leu Cys His Asn Met	Asn Ile Trp Gly Gln Ile			
	185	190			195
Trp Pro Lys Ala	Val Tyr Leu Val Cys	Asn Tyr Ser Pro Lys Gly			
	200	205			210
Asn Trp Trp Gly	His Ala Pro Tyr Lys	His Gly Arg Pro Cys Ser			
	215	220			225
Ala Cys Pro Pro	Ser Phe Gly Gly Gly	Cys Arg Glu Asn Leu Cys			
	230	235			240
Tyr Lys Glu Gly	Ser Asp Arg Tyr Tyr	Pro Pro Arg Glu Glu Glu			
	245	250			255
Thr Asn Glu Ile	Glu Arg Gln Gln Ser	Gln Val His Asp Thr His			
	260	265			270
Val Arg Thr Arg	Ser Asp Asp Ser Ser	Arg Asn Glu Val Ile Ser			
	275	280			285
Ala Gln Gln Met	Ser Gln Ile Val Ser	Cys Glu Val Arg Leu Arg			
	290	295			300
Asp Gln Cys Lys	Gly Thr Thr Cys Asn	Arg Tyr Glu Cys Pro Ala			
	305	310			315
Gly Cys Leu Asp	Ser Lys Ala Lys Val	Ile Gly Ser Val His Tyr			
	320	325			330
Glu Met Gln Ser	Ser Ile Cys Arg Ala	Ala Ile His Tyr Gly Ile			
	335	340			345
Ile Asp Asn Asp	Gly Gly Trp Val Asp	Ile Thr Arg Gln Gly Arg			
	350	355			360
Lys His Tyr Phe	Ile Lys Ser Asn Arg	Asn Gly Ile Gln Thr Ile			
	365	370			375
Gly Lys Tyr Gln	Ser Ala Asn Ser Phe	Thr Val Ser Lys Val Thr			
	380	385			390
Val Gln Ala Val	Thr Cys Glu Thr Thr	Val Glu Gln Leu Cys Pro			
	395	400			405
Phe His Lys Pro	Ala Ser His Cys Pro	Arg Val Tyr Cys Pro Arg			
	410	415			420
Asn Cys Met Gln	Ala Asn Pro His Tyr	Ala Arg Val Ile Gly Thr			
	425	430			435
Arg Val Tyr Ser	Asp Leu Ser Ser Ile	Cys Arg Ala Ala Val His			
	440	445			450
Ala Gly Val Val	Arg Asn His Gly Gly	Tyr Val Asp Val Met Pro			
	455	460			465

Val	Asp	Lys	Arg	Lys	Thr	Tyr	Ile	Ala	Ser	Phe	Gln	Asn	Gly	Ile
				470					475					480
Phe	Ser	Glu	Ser	Leu	Gln	Asn	Pro	Pro	Gly	Gly	Lys	Ala	Phe	Arg
				485					490					495
Val	Phe	Ala	Val	Val										
				500										

<210> 364

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 364

ggacagaatt tgggagcaca ctgg 24

<210> 365

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 365

ccaagagtat actgtcctcg 20

<210> 366

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 366

agcacagatt ttctctacag ccccc 25

<210> 367

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 367

aaccactcca gcatgtactg ctgc 24

<210> 368

<211> 50

<212> DNA

<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 368  
ccattcaggt gttctggccc tgtatgtaca cattatacac aggtcgtgtg 50

<210> 369  
<211> 1685  
<212> DNA

<213> Homo sapiens

<400> 369  
gcggagacaa gcgcagagcg cagcgcacgg ccacagacag ccctgggcat 50  
ccaccgacgg cgcagccgga gccagcagag ccggaaggcg cgccccgggc 100  
agagaaagcc gagcagagct ggggtggcgtc tccggggccgc cgctccgacg 150  
ggccagcggc ctccccatgt ccctgctccc acgccgcgcc cctccgggtca 200  
gcatgaggct cctggcggcc gcgctgctcc tgctgctgct ggcgctgtac 250  
accgcgcgtg tggacggggtc caaatgcaag tgctcccgga agggacccaa 300  
gatccgctac agcgacgtga agaagctgga aatgaagcca aagtaccgcg 350  
actgcgagga gaagatggtt atcatcacca ccaagagcgt gtccaggtag 400  
cgaggtcagg agcactgcct gcaccccaag ctgcagagca ccaagcgctt 450  
catcaagtgg tacaacgcct ggaacgagaa gcgcaggggtc tacgaagaat 500  
agggtgaaaa acctcagaag ggaaaactcc aaaccagttg ggagacttgt 550  
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<211> 111

<212> PRT

<213> Homo sapiens

<400> 370

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				20					25					30
Arg	Val	Asp	Gly	Ser	Lys	Cys	Lys	Cys	Ser	Arg	Lys	Gly	Pro	Lys
				35					40					45
Ile	Arg	Tyr	Ser	Asp	Val	Lys	Lys	Leu	Glu	Met	Lys	Pro	Lys	Tyr
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Pro	His	Cys	Glu	Glu	Lys	Met	Val	Ile	Ile	Thr	Thr	Lys	Ser	Val
				65					70					75
Ser	Arg	Tyr	Arg	Gly	Gln	Glu	His	Cys	Leu	His	Pro	Lys	Leu	Gln
				80					85					90
Ser	Thr	Lys	Arg	Phe	Ile	Lys	Trp	Tyr	Asn	Ala	Trp	Asn	Glu	Lys
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<223> Synthetic oligonucleotide probe

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<223> Synthetic oligonucleotide probe

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<212> DNA

<213> Homo sapiens

<400> 374

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cggtttcagc cccagaacc cccgtcctcc tggactggca tccgaaatac 300

tactcagttt gctgctgtgt gccccagca cctggatgag agatccttac 350

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gtaatgaccg tgggtgaagac gaagatattc atgatcagaa cagtaagaag 550

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Ser	Ser	Trp	Thr	Gly	Ile	Arg	Asn	Thr	Thr	Gln	Phe	Ala	Ala	Val
				80					85					90
Cys	Pro	Gln	His	Leu	Asp	Glu	Arg	Ser	Leu	Leu	His	Asp	Met	Leu
				95					100					105
Pro	Ile	Trp	Phe	Thr	Ala	Asn	Leu	Asp	Thr	Leu	Met	Thr	Tyr	Val
				110					115					120
Gln	Asp	Gln	Asn	Glu	Asp	Cys	Leu	Tyr	Leu	Asn	Ile	Tyr	Val	Pro
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Thr	Glu	Asp	Gly	Ala	Asn	Thr	Lys	Lys	Asn	Ala	Asp	Asp	Ile	Thr
				140					145					150
Ser	Asn	Asp	Arg	Gly	Glu	Asp	Glu	Asp	Ile	His	Asp	Gln	Asn	Ser
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Lys	Lys	Pro	Val	Met	Val	Tyr	Ile	His	Gly	Gly	Ser	Tyr	Met	Glu
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Gly	Thr	Gly	Asn	Met	Ile	Asp	Gly	Ser	Ile	Leu	Ala	Ser	Tyr	Gly
				185					190					195
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				200					205					210
Phe	Leu	Ser	Thr	Gly	Asp	Gln	Ala	Ala	Lys	Gly	Asn	Tyr	Gly	Leu
				215					220					225
Leu	Asp	Gln	Ile	Gln	Ala	Leu	Arg	Trp	Ile	Glu	Glu	Asn	Val	Gly
				230					235					240
Ala	Phe	Gly	Gly	Asp	Pro	Lys	Arg	Val	Thr	Ile	Phe	Gly	Ser	Gly
				245					250					255
Ala	Gly	Ala	Ser	Cys	Val	Ser	Leu	Leu	Thr	Leu	Ser	His	Tyr	Ser
				260					265					270
Glu	Gly	Leu	Phe	Gln	Lys	Ala	Ile	Ile	Gln	Ser	Gly	Thr	Ala	Leu
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Ser	Ser	Trp	Ala	Val	Asn	Tyr	Gln	Pro	Ala	Lys	Tyr	Thr	Arg	Ile
				290					295					300
Leu	Ala	Asp	Lys	Val	Gly	Cys	Asn	Met	Leu	Asp	Thr	Thr	Asp	Met
				305					310					315
Val	Glu	Cys	Leu	Arg	Asn	Lys	Asn	Tyr	Lys	Glu	Leu	Ile	Gln	Gln
				320					325					330
Thr	Ile	Thr	Pro	Ala	Thr	Tyr	His	Ile	Ala	Phe	Gly	Pro	Val	Ile
				335					340					345

Asp Gly Asp Val	Ile Pro Asp Asp Pro	Gln Ile Leu Met Glu Gln	350	355	360
Gly Glu Phe Leu	Asn Tyr Asp Ile Met	Leu Gly Val Asn Gln Gly	365	370	375
Glu Gly Leu Lys	Phe Val Asp Gly Ile	Val Asp Asn Glu Asp Gly	380	385	390
Val Thr Pro Asn	Asp Phe Asp Phe Ser	Val Ser Asn Phe Val Asp	395	400	405
Asn Leu Tyr Gly	Tyr Pro Glu Gly Lys	Asp Thr Leu Arg Glu Thr	410	415	420
Ile Lys Phe Met	Tyr Thr Asp Trp Ala	Asp Lys Glu Asn Pro Glu	425	430	435
Thr Arg Arg Lys	Thr Leu Val Ala Leu	Phe Thr Asp His Gln Trp	440	445	450
Val Ala Pro Ala	Val Ala Ala Asp Leu	His Ala Gln Tyr Gly Ser	455	460	465
Pro Thr Tyr Phe	Tyr Ala Phe Tyr His	His Cys Gln Ser Glu Met	470	475	480
Lys Pro Ser Trp	Ala Asp Ser Ala His	Gly Asp Glu Val Pro Tyr	485	490	495
Val Phe Gly Ile	Pro Met Ile Gly Pro	Thr Glu Leu Phe Ser Cys	500	505	510
Asn Phe Ser Lys	Asn Asp Val Met Leu	Ser Ala Val Val Met Thr	515	520	525
Tyr Trp Thr Asn	Phe Ala Lys Thr Gly	Asp Pro Asn Gln Pro Val	530	535	540
Pro Gln Asp Thr	Lys Phe Ile His Thr	Lys Pro Asn Arg Phe Glu	545	550	555
Glu Val Ala Trp	Ser Lys Tyr Asn Pro	Lys Asp Gln Leu Tyr Leu	560	565	570
His Ile Gly Leu	Lys Pro Arg Val Arg	Asp His Tyr Arg Ala Thr	575	580	585
Lys Val Ala Phe	Trp Leu Glu Leu Val	Pro His Leu His Asn Leu	590	595	600
Asn Glu Ile Phe	Gln Tyr Val Ser Thr	Thr Thr Lys Val Pro Pro	605	610	615
Pro Asp Met Thr	Ser Phe Pro Tyr Gly	Thr Arg Arg Ser Pro Ala	620	625	630
Lys Ile Trp Pro	Thr Thr Lys Arg Pro	Ala Ile Thr Pro Ala Asn			

635	640	645
Asn Pro Lys His Ser Lys Asp Pro His	Lys Thr Gly Pro Glu Asp	
650	655	660
Thr Thr Val Leu Ile Glu Thr Lys Arg	Asp Tyr Ser Thr Glu Leu	
665	670	675
Ser Val Thr Ile Ala Val Gly Ala Ser	Leu Leu Phe Leu Asn Ile	
680	685	690
Leu Ala Phe Ala Ala Leu Tyr Tyr Lys	Lys Asp Lys Arg Arg His	
695	700	705
Glu Thr His Arg Arg Pro Ser Pro Gln	Arg Asn Thr Thr Asn Asp	
710	715	720
Ile Ala His Ile Gln Asn Glu Glu Ile	Met Ser Leu Gln Met Lys	
725	730	735
Gln Leu Glu His Asp His Glu Cys Glu	Ser Leu Gln Ala His Asp	
740	745	750
Thr Leu Arg Leu Thr Cys Pro Pro Asp	Tyr Thr Leu Thr Leu Arg	
755	760	765
Arg Ser Pro Asp Asp Ile Pro Leu Met	Thr Pro Asn Thr Ile Thr	
770	775	780
Met Ile Pro Asn Thr Leu Thr Gly Met	Gln Pro Leu His Thr Phe	
785	790	795
Asn Thr Phe Ser Gly Gly Gln Asn Ser	Thr Asn Leu Pro His Gly	
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<211> 246

<212> DNA

<213> Hom

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**DEBATE**

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—

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□ □ □ □ □ □ □ □ □ □

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atgtcatt

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<212> PRT

<213> Homo sapiens

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Leu	Leu	Leu	Gly	Ser	Gly	Gln	Gly	Pro	Gln	Gln	Val	Gly	Ala	Gly
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Gln	Thr	Phe	Glu	Tyr	Leu	Lys	Arg	Glu	His	Ser	Leu	Ser	Lys	Pro
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Tyr	Gln	Gly	Val	Gly	Thr	Gly	Ser	Ser	Ser	Leu	Trp	Asn	Leu	Met
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Gly	Asn	Ala	Met	Val	Met	Thr	Gln	Tyr	Ile	Arg	Leu	Thr	Pro	Asp
				80					85					90
Met	Gln	Ser	Lys	Gln	Gly	Ala	Leu	Trp	Asn	Arg	Val	Pro	Cys	Phe
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Leu	Arg	Asp	Trp	Glu	Leu	Gln	Val	His	Phe	Lys	Ile	His	Gly	Gln
				110					115					120
Gly	Lys	Lys	Asn	Leu	His	Gly	Asp	Gly	Leu	Ala	Ile	Trp	Tyr	Thr
				125					130					135
Lys	Asp	Arg	Met	Gln	Pro	Gly	Pro	Val	Phe	Gly	Asn	Met	Asp	Lys
				140					145					150
Phe	Val	Gly	Leu	Gly	Val	Phe	Val	Asp	Thr	Tyr	Pro	Asn	Glu	Glu
				155					160					165
Lys	Gln	Gln	Glu	Arg	Val	Phe	Pro	Tyr	Ile	Ser	Ala	Met	Val	Asn
				170					175					180
Asn	Gly	Ser	Leu	Ser	Tyr	Asp	His	Glu	Arg	Asp	Gly	Arg	Pro	Thr
				185					190					195
Glu	Leu	Gly	Gly	Cys	Thr	Ala	Ile	Val	Arg	Asn	Leu	His	Tyr	Asp
				200					205					210
Thr	Phe	Leu	Val	Ile	Arg	Tyr	Val	Lys	Arg	His	Leu	Thr	Ile	Met
				215					220					225
Met	Asp	Ile	Asp	Gly	Lys	His	Glu	Trp	Arg	Asp	Cys	Ile	Glu	Val
				230					235					240
Pro	Gly	Val	Arg	Leu	Pro	Arg	Gly	Tyr	Tyr	Phe	Gly	Thr	Ser	Ser
				245					250					255

Ile Thr Gly Asp Leu Ser Asp Asn His Asp Val Ile Ser Leu Lys	260	265	270
Leu Phe Glu Leu Thr Val Glu Arg Thr Pro Glu Glu Glu Lys Leu	275	280	285
His Arg Asp Val Phe Leu Pro Ser Val Asp Asn Met Lys Leu Pro	290	295	300
Glu Met Thr Ala Pro Leu Pro Pro Leu Ser Gly Leu Ala Leu Phe	305	310	315
Leu Ile Val Phe Phe Ser Leu Val Phe Ser Val Phe Ala Ile Val	320	325	330
Ile Gly Ile Ile Leu Tyr Asn Lys Trp Gln Glu Gln Ser Arg Lys	335	340	345

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<220>  
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<400> 382  
 cactctccag gctgcatgct cagg 24

<210> 383  
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<400> 383  
 gtcaaacgtt cgagtacttg aaacgggagc actcgctgtc gaagc 45

<210> 384  
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				215					220					225	
Asp	Trp	Lys	Lys	Ile	Tyr	Phe	Arg	His	Gln	Pro	Ser	Ala	Leu	Phe	
				230					235					240	
Cys	Ser	Gly	Ser	Cys	Tyr	Cys	Pro	Val	Arg	Asn	Gln	Tyr	Leu	Glu	
				245					250					255	
Lys	Glu	Gln	Arg	Arg	Gln	Tyr	Leu	Leu	Arg	Leu	Lys	Asn	Ser	Gln	
				260					265					270	
Leu	Glu	Lys	Thr	Tyr	Gly	Glu	Met	Ala	Lys	Ile	Val	Asp	Val	Pro	
				275					280					285	
Thr	Lys	Gln	Leu	Arg	Ala	Ala	Asn	Pro	Ile	Asp	Ser	Met	Leu	Cys	
				290					295					300	
His	Phe	Cys	His	Asn	Val	Ser	Phe	Pro	Cys	Thr	Arg	Asn	Gly	Cys	
				305					310					315	
Val	Asp	Met	Glu	His	Phe	Lys	Val	Ile	Lys	Thr	His	Gln	Ile	Glu	
				320					325					330	
Asp	Glu	Arg	Glu	Arg	Arg	Glu	Lys	Lys	Leu	Tyr	Phe	Gly	Tyr	Ser	
				335					340					345	
Leu	Leu	Gly	Ala	His	Pro	Ile	Leu	Asn	Gln	Thr	Ile	Gly	Arg	Met	
				350					355					360	
Gln	Arg	Ala	Thr	Glu	Gly	Arg	Lys	Glu	Glu	Leu	Phe	Ala	Leu	Tyr	
				365					370					375	
Ser	Ala	His	Asp	Val	Thr	Leu	Ser	Pro	Val	Leu	Ser	Ala	Leu	Gly	
				380					385					390	
Leu	Ser	Glu	Ala	Arg	Phe	Pro	Arg	Phe	Ala	Ala	Arg	Leu	Ile	Phe	
				395					400					405	
Glu	Leu	Trp	Gln	Asp	Arg	Glu	Lys	Pro	Ser	Glu	His	Ser	Val	Arg	
				410					415					420	
Ile	Leu	Tyr	Asn	Gly	Val	Asp	Val	Thr	Phe	His	Thr	Ser	Phe	Cys	
				425					430					435	
Gln	Asp	His	His	Lys	Arg	Ser	Pro	Lys	Pro	Met	Cys	Pro	Leu	Glu	
				440					445					450	
Asn	Leu	Val	Arg	Phe	Val	Lys	Arg	Asp	Met	Phe	Val	Ala	Leu	Gly	
				455					460					465	
Gly	Ser	Gly	Thr	Asn	Tyr	Tyr	Asp	Ala	Cys	His	Arg	Glu	Gly	Phe	
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<210> 386

<211> 24

<212> DNA

<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 386  
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<210> 387  
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<220>  
<223> Synthetic oligonucleotide probe

<400> 387  
ttccctatgc tctgtattgg catgg 25

<210> 388  
<211> 50  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 388  
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<210> 389  
<211> 3313  
<212> DNA  
<213> Homo sapiens

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cccttttgaa gaacagtact gtggagctat ttaagagata aaaacgaaat 100  
atcctttctg ggagttcaag attgtgcagt aattggttag gactctgagc 150  
gccgctgttc accaatcggg gagagaaaag cggagatcct gctcgccttg 200  
cacgcgcctg aagcaciaag cagatagcta ggaatgaacc atccctggga 250  
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gggcgaagga actgctcctg acttcagtgg ttaagggcag aattgaaaat 350  
aattctggag gaagataaga atgattcctg cgcgactgca ccgggactac 400  
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atgcacccag atacgctatt cagttccgga agagctggag aaaggctcta 500  
gggtgggcga catctccagg gacctggggc tggagccccg ggagctcgcg 550  
gagcgcggag tccgcatcat cccagaggt aggacgcagc ttttcgcct 600



gaatccgcgc agcggcagct tggtcacggc gggcaggata gaccgggagg 650  
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 gaggataaag tgaaaatata tggagtagaa gtagaagtaa gggacattaa 750  
 cgacaatgcg ccttactttc gtgaaagtga attagaaata aaaattagtg 800  
 aaaatgcagc cactgagatg cggttccctc taccacacgc ctgggatccg 850  
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 cttctccctc atcgtgcaaa atggagccga cggtagtaag taccocgaat 950  
 tggtgctgaa acgcgcctg gaccgcgaag aaaaggctgc tcaccacctg 1000  
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 aaaaatacaa aattagccgg gcgtggtggt gcatgtctgt aatcccagct 3200  
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 aaactctatc tca 3313

<210> 390  
 <211> 916  
 <212> PRT  
 <213> Homo sapiens  
 <400> 390

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Leu	Gly	Ile	Leu	Leu	Gly	Thr	Leu	Trp	Glu	Thr	Gly	Cys	Thr	Gln		20	25	30	
Ile	Arg	Tyr	Ser	Val	Pro	Glu	Glu	Leu	Glu	Lys	Gly	Ser	Arg	Val		35	40	45	
Gly	Asp	Ile	Ser	Arg	Asp	Leu	Gly	Leu	Glu	Pro	Arg	Glu	Leu	Ala		50	55	60	
Glu	Arg	Gly	Val	Arg	Ile	Ile	Pro	Arg	Gly	Arg	Thr	Gln	Leu	Phe		65	70	75	
Ala	Leu	Asn	Pro	Arg	Ser	Gly	Ser	Leu	Val	Thr	Ala	Gly	Arg	Ile		80	85	90	
Asp	Arg	Glu	Glu	Leu	Cys	Met	Gly	Ala	Ile	Lys	Cys	Gln	Leu	Asn		95	100	105	
Leu	Asp	Ile	Leu	Met	Glu	Asp	Lys	Val	Lys	Ile	Tyr	Gly	Val	Glu		110	115	120	
Val	Glu	Val	Arg	Asp	Ile	Asn	Asp	Asn	Ala	Pro	Tyr	Phe	Arg	Glu		125	130	135	
Ser	Glu	Leu	Glu	Ile	Lys	Ile	Ser	Glu	Asn	Ala	Ala	Thr	Glu	Met		140	145	150	
Arg	Phe	Pro	Leu	Pro	His	Ala	Trp	Asp	Pro	Asp	Ile	Gly	Lys	Asn		155	160	165	
Ser	Leu	Gln	Ser	Tyr	Glu	Leu	Ser	Pro	Asn	Thr	His	Phe	Ser	Leu		170	175	180	
Ile	Val	Gln	Asn	Gly	Ala	Asp	Gly	Ser	Lys	Tyr	Pro	Glu	Leu	Val		185	190	195	
Leu	Lys	Arg	Ala	Leu	Asp	Arg	Glu	Glu	Lys	Ala	Ala	His	His	Leu		200	205	210	
Val	Leu	Thr	Ala	Ser	Asp	Gly	Gly	Asp	Pro	Val	Arg	Thr	Gly	Thr		215	220	225	
Ala	Arg	Ile	Arg	Val	Met	Val	Leu	Asp	Ala	Asn	Asp	Asn	Ala	Pro		230	235	240	
Ala	Phe	Ala	Gln	Pro	Glu	Tyr	Arg	Ala	Ser	Val	Pro	Glu	Asn	Leu		245	250	255	
Ala	Leu	Gly	Thr	Gln	Leu	Leu	Val	Val	Asn	Ala	Thr	Asp	Pro	Asp		260	265	270	
Glu	Gly	Val	Asn	Ala	Glu	Val	Arg	Tyr	Ser	Phe	Arg	Tyr	Val	Asp		275	280	285	
Asp	Lys	Ala	Ala	Gln	Val	Phe	Lys	Leu	Asp	Cys	Asn	Ser	Gly	Thr					

	290	295	300
Ile Ser Thr Ile	Gly Glu Leu Asp His 305	Glu Glu Ser Gly Phe 310	Tyr 315
Gln Met Glu Val	Gln Ala Met Asp Asn 320	Ala Gly Tyr Ser Ala 325	Arg 330
Ala Lys Val Leu	Ile Thr Val Leu Asp 335	Val Asn Asp Asn Ala 340	Pro 345
Glu Val Val Leu	Thr Ser Leu Ala Ser 350	Ser Val Pro Glu Asn 355	Ser 360
Pro Arg Gly Thr	Leu Ile Ala Leu Leu 365	Asn Val Asn Asp Gln 370	Asp 375
Ser Glu Glu Asn	Gly Gln Val Ile Cys 380	Phe Ile Gln Gly Asn 385	Leu 390
Pro Phe Lys Leu	Glu Lys Ser Tyr Gly 395	Asn Tyr Tyr Ser Leu 400	Val 405
Thr Asp Ile Val	Leu Asp Arg Glu Gln 410	Val Pro Ser Tyr Asn 415	Ile 420
Thr Val Thr Ala	Thr Asp Arg Gly Thr 425	Pro Pro Leu Ser Thr 430	Glu 435
Thr His Ile Ser	Leu Asn Val Ala Asp 440	Thr Asn Asp Asn Pro 445	Pro 450
Val Phe Pro Gln	Ala Ser Tyr Ser Ala 455	Tyr Ile Pro Glu Asn 460	Asn 465
Pro Arg Gly Val	Ser Leu Val Ser Val 470	Thr Ala His Asp Pro 475	Asp 480
Cys Glu Glu Asn	Ala Gln Ile Thr Tyr 485	Ser Leu Ala Glu Asn 490	Thr 495
Ile Gln Gly Ala	Ser Leu Ser Ser Tyr 500	Val Ser Ile Asn Ser 505	Asp 510
Thr Gly Val Leu	Tyr Ala Leu Ser Ser 515	Phe Asp Tyr Glu Gln 520	Phe 525
Arg Asp Leu Gln	Val Lys Val Met Ala 530	Arg Asp Asn Gly His 535	Pro 540
Pro Leu Ser Ser	Asn Val Ser Leu Ser 545	Leu Phe Val Leu Asp 550	Gln 555
Asn Asp Asn Ala	Pro Glu Ile Leu Tyr 560	Pro Ala Leu Pro Thr 565	Asp 570
Gly Ser Thr Gly	Val Glu Leu Ala Pro 575	Arg Ser Ala Glu Pro 580	Gly 585

Tyr	Leu	Val	Thr	Lys	Val	Val	Ala	Val	Asp	Arg	Asp	Ser	Gly	Gln	590	595	600
Asn	Ala	Trp	Leu	Ser	Tyr	Arg	Leu	Leu	Lys	Ala	Ser	Glu	Pro	Gly	605	610	615
Leu	Phe	Ser	Val	Gly	Leu	His	Thr	Gly	Glu	Val	Arg	Thr	Ala	Arg	620	625	630
Ala	Leu	Leu	Asp	Arg	Asp	Ala	Leu	Lys	Gln	Ser	Leu	Val	Val	Ala	635	640	645
Val	Gln	Asp	His	Gly	Gln	Pro	Pro	Leu	Ser	Ala	Thr	Val	Thr	Leu	650	655	660
Thr	Val	Ala	Val	Ala	Asp	Ser	Ile	Pro	Gln	Val	Leu	Ala	Asp	Leu	665	670	675
Gly	Ser	Leu	Glu	Ser	Pro	Ala	Asn	Ser	Glu	Thr	Ser	Asp	Leu	Thr	680	685	690
Leu	Tyr	Leu	Val	Val	Ala	Val	Ala	Ala	Val	Ser	Cys	Val	Phe	Leu	695	700	705
Ala	Phe	Val	Ile	Leu	Leu	Leu	Ala	Leu	Arg	Leu	Arg	Arg	Trp	His	710	715	720
Lys	Ser	Arg	Leu	Leu	Gln	Ala	Ser	Gly	Gly	Gly	Leu	Thr	Gly	Ala	725	730	735
Pro	Ala	Ser	His	Phe	Val	Gly	Val	Asp	Gly	Val	Gln	Ala	Phe	Leu	740	745	750
Gln	Thr	Tyr	Ser	His	Glu	Val	Ser	Leu	Thr	Thr	Asp	Ser	Arg	Lys	755	760	765
Ser	His	Leu	Ile	Phe	Pro	Gln	Pro	Asn	Tyr	Ala	Asp	Met	Leu	Val	770	775	780
Ser	Gln	Glu	Ser	Phe	Glu	Lys	Ser	Glu	Pro	Leu	Leu	Leu	Ser	Gly	785	790	795
Asp	Ser	Val	Phe	Ser	Lys	Asp	Ser	His	Gly	Leu	Ile	Glu	Val	Ser	800	805	810
Leu	Tyr	Gln	Ile	Phe	Phe	Leu	Phe	Phe	Phe	Asn	Cys	Ser	Val	Ser	815	820	825
Gln	Ala	Gly	Val	Gln	Arg	Tyr	Asp	His	Ser	Ser	Leu	Arg	Pro	Gln	830	835	840
Thr	Pro	Arg	Leu	Lys	Gln	Leu	Ser	His	Leu	Cys	Leu	Arg	Cys	Asn	845	850	855
Arg	Asp	Tyr	Arg	Cys	Lys	Pro	Pro	Thr	Val	Cys	Leu	Ser	Ile	Tyr	860	865	870
Leu	Ser	Ile	Tyr	Leu	Ser	Ile	Tyr	Leu	Ser	Ile	Tyr	Leu	Leu	Leu			

	875		880		885
Ser Cys Thr Asp Gly Ser Leu Thr Pro Val Ile Pro Val Leu Trp					
	890		895		900
Glu Ala Glu Ala Gly Gly Ser Pro Glu Val Gly Ser Leu Arg Pro					
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<210> 391

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 391

tccgtctctg tgaaccgccc cac 23

<210> 392

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 392

ctcgggcgca ttgtcgttct ggtc 24

<210> 393

<211> 40

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 393

ccgactgtga aagagaacgc cccagatcca cttgttcccc 40

<210> 394

<211> 999

<212> DNA

<213> Homo sapiens

<400> 394

cccaggctct agtgcaggag gagaaggagg aggagcagga ggtggagatt 50

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ggggcctcct cactgggtc cgaatcagta ggtgaccccg cccctggatt 150

ctggaagacc tcaccatggg acgccccga cctcgtgcgg ccaagacgtg 200

gatgttcctg ctcttgctgg ggggagcctg ggcaggacac tccagggcac 250  
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 caagaaatac ctgtggttca gtccatccca caccctgtct acaacagcag 500  
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 gctcagaccc ctgtgggagg tccgacaaac ctggcgtcta taccaacatc 900  
 tgccgctacc tggactggat caagaagatc ataggcagca agggctgatt 950  
 ctaggataag cactagatct cccttaataa actcacaact ctctgggttc 999

<210> 395

<211> 260

<212> PRT

<213> Homo sapiens

<400> 395

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Leu	Leu	Leu	Gly	Gly	Ala	Trp	Ala	Gly	His	Ser	Arg	Ala	Gln	Glu
			20						25					30
Asp	Lys	Val	Leu	Gly	Gly	His	Glu	Cys	Gln	Pro	His	Ser	Gln	Pro
			35						40					45
Trp	Gln	Ala	Ala	Leu	Phe	Gln	Gly	Gln	Gln	Leu	Leu	Cys	Gly	Gly
			50						55					60
Val	Leu	Val	Gly	Gly	Asn	Trp	Val	Leu	Thr	Ala	Ala	His	Cys	Lys
			65						70					75
Lys	Pro	Lys	Tyr	Thr	Val	Arg	Leu	Gly	Asp	His	Ser	Leu	Gln	Asn
			80						85					90
Lys	Asp	Gly	Pro	Glu	Gln	Glu	Ile	Pro	Val	Val	Gln	Ser	Ile	Pro
			95						100					105

His	Pro	Cys	Tyr	Asn	Ser	Ser	Asp	Val	Glu	Asp	His	Asn	His	Asp
				110					115					120
Leu	Met	Leu	Leu	Gln	Leu	Arg	Asp	Gln	Ala	Ser	Leu	Gly	Ser	Lys
				125					130					135
Val	Lys	Pro	Ile	Ser	Leu	Ala	Asp	His	Cys	Thr	Gln	Pro	Gly	Gln
				140					145					150
Lys	Cys	Thr	Val	Ser	Gly	Trp	Gly	Thr	Val	Thr	Ser	Pro	Arg	Glu
				155					160					165
Asn	Phe	Pro	Asp	Thr	Leu	Asn	Cys	Ala	Glu	Val	Lys	Ile	Phe	Pro
				170					175					180
Gln	Lys	Lys	Cys	Glu	Asp	Ala	Tyr	Pro	Gly	Gln	Ile	Thr	Asp	Gly
				185					190					195
Met	Val	Cys	Ala	Gly	Ser	Ser	Lys	Gly	Ala	Asp	Thr	Cys	Gln	Gly
				200					205					210
Asp	Ser	Gly	Gly	Pro	Leu	Val	Cys	Asp	Gly	Ala	Leu	Gln	Gly	Ile
				215					220					225
Thr	Ser	Trp	Gly	Ser	Asp	Pro	Cys	Gly	Arg	Ser	Asp	Lys	Pro	Gly
				230					235					240
Val	Tyr	Thr	Asn	Ile	Cys	Arg	Tyr	Leu	Asp	Trp	Ile	Lys	Lys	Ile
				245					250					255
Ile	Gly	Ser	Lys	Gly										
				260										

<210> 396  
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 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 396  
 cagcctacag aataaagatg gccc 24

<210> 397  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 397  
 ggtgcaatga tctgccaggc tgat 24

<210> 398  
 <211> 48  
 <212> DNA



<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 398

agaaatacct gtggttcagt ccatcccaaa cccctgctac aacagcag 48

<210> 399

<211> 2236

<212> DNA

<213> Homo sapiens

<400> 399

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cgccgcgagg ccccgccccg gcccgcccc gcccgcccc ggccggcggg 200  
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cccaaccct acgatgaaga gggcgccgc tggagggagc cggctgctgg 550  
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tgccgcaacc tcaccatcct gtggctgcac tcgaatgtgc tggcccgaat 800  
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cccggggctg ttccgcggcc tggctgccct gcagtacctc tacctgcagg 1000  
acaacgcgct gcaggcactg cctgatgaca ccttccgcga cctgggcaac 1050  
ctcacacacc tcttcctgca cggcaaccgc atctccagcg tgcccgagcg 1100



Cys	Val	Cys	Tyr	Asn	Glu	Pro	Lys	Val	Thr	Thr	Ser	Cys	Pro	Gln	
				35					40					45	
Gln	Gly	Leu	Gln	Ala	Val	Pro	Val	Gly	Ile	Pro	Ala	Ala	Ser	Gln	
				50					55					60	
Arg	Ile	Phe	Leu	His	Gly	Asn	Arg	Ile	Ser	His	Val	Pro	Ala	Ala	
				65					70					75	
Ser	Phe	Arg	Ala	Cys	Arg	Asn	Leu	Thr	Ile	Leu	Trp	Leu	His	Ser	
				80					85					90	
Asn	Val	Leu	Ala	Arg	Ile	Asp	Ala	Ala	Ala	Phe	Thr	Gly	Leu	Ala	
				95					100					105	
Leu	Leu	Glu	Gln	Leu	Asp	Leu	Ser	Asp	Asn	Ala	Gln	Leu	Arg	Ser	
				110					115					120	
Val	Asp	Pro	Ala	Thr	Phe	His	Gly	Leu	Gly	Arg	Leu	His	Thr	Leu	
				125					130					135	
His	Leu	Asp	Arg	Cys	Gly	Leu	Gln	Glu	Leu	Gly	Pro	Gly	Leu	Phe	
				140					145					150	
Arg	Gly	Leu	Ala	Ala	Leu	Gln	Tyr	Leu	Tyr	Leu	Gln	Asp	Asn	Ala	
				155					160					165	
Leu	Gln	Ala	Leu	Pro	Asp	Asp	Thr	Phe	Arg	Asp	Leu	Gly	Asn	Leu	
				170					175					180	
Thr	His	Leu	Phe	Leu	His	Gly	Asn	Arg	Ile	Ser	Ser	Val	Pro	Glu	
				185					190					195	
Arg	Ala	Phe	Arg	Gly	Leu	His	Ser	Leu	Asp	Arg	Leu	Leu	Leu	His	
				200					205					210	
Gln	Asn	Arg	Val	Ala	His	Val	His	Pro	His	Ala	Phe	Arg	Asp	Leu	
				215					220					225	
Gly	Arg	Leu	Met	Thr	Leu	Tyr	Leu	Phe	Ala	Asn	Asn	Leu	Ser	Ala	
				230					235					240	
Leu	Pro	Thr	Glu	Ala	Leu	Ala	Pro	Leu	Arg	Ala	Leu	Gln	Tyr	Leu	
				245					250					255	
Arg	Leu	Asn	Asp	Asn	Pro	Trp	Val	Cys	Asp	Cys	Arg	Ala	Arg	Pro	
				260					265					270	
Leu	Trp	Ala	Trp	Leu	Gln	Lys	Phe	Arg	Gly	Ser	Ser	Ser	Glu	Val	
				275					280					285	
Pro	Cys	Ser	Leu	Pro	Gln	Arg	Leu	Ala	Gly	Arg	Asp	Leu	Lys	Arg	
				290					295					300	
Leu	Ala	Ala	Asn	Asp	Leu	Gln	Gly	Cys	Ala	Val	Ala	Thr	Gly	Pro	
				305					310					315	
Tyr	His	Pro	Ile	Trp	Thr	Gly	Arg	Ala	Thr	Asp	Glu	Glu	Pro	Leu	

320	325	330
Gly Leu Pro Lys Cys Cys Gln Pro Asp	Ala Ala Asp Lys Ala Ser	
335	340	345
Val Leu Glu Pro Gly Arg Pro Ala Ser	Ala Gly Asn Ala Leu Lys	
350	355	360
Gly Arg Val Pro Pro Gly Asp Ser Pro	Pro Gly Asn Gly Ser Gly	
365	370	375
Pro Arg His Ile Asn Asp Ser Pro Phe	Gly Thr Leu Pro Gly Ser	
380	385	390
Ala Glu Pro Pro Leu Thr Ala Val Arg	Pro Glu Gly Ser Glu Pro	
395	400	405
Pro Gly Phe Pro Thr Ser Gly Pro Arg	Arg Arg Pro Gly Cys Ser	
410	415	420
Arg Lys Asn Arg Thr Arg Ser His Cys	Arg Leu Gly Gln Ala Gly	
425	430	435
Ser Gly Gly Gly Gly Thr Gly Asp Ser	Glu Gly Ser Gly Ala Leu	
440	445	450
Pro Ser Leu Thr Cys Ser Leu Thr Pro	Leu Gly Leu Ala Leu Val	
455	460	465
Leu Trp Thr Val Leu Gly Pro Cys		
470		

<210> 401  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 401  
 tggctgccct gcagtacctc tacc 24

<210> 402  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 402  
 ccctgcaggt cattggcagc tagg 24

<210> 403  
 <211> 45  
 <212> DNA  
 <213> Artificial Sequence



cttttctgga aaatgcaccg ttctgattca agtgatagat gtgaacgacc 1200  
 atgccccaga agttaccatg tctgcattta ccagcccaat acctgagaac 1250  
 gcgcctgaaa ctgtggttgc acttttcagt gtttcagatc ttgattcagg 1300  
 agaaaatggg aaaattagtt gctccattca ggaggatcta cccttcctcc 1350  
 tgaaatccgc ggaaaacttt tacaccctac taacggagag accactagac 1400  
 agagaaagca gagcggaata caacatcact atcactgtca ctgacttggg 1450  
 gacccttatg ctgataacac agctcaatat gaccgtgctg atcgccgatg 1500  
 tcaatgacaa cgctcccgcc ttcacccaaa cctcctacac cctgttcgtc 1550  
 cgcgagaaca acagccccgc cctgcacatc cgcagcgtca gcgctacaga 1600  
 cagagactca ggcaccaacg cccaggtcac ctactcgctg ctgccgcccc 1650  
 aggacccgca cctgcccctc acatccctgg tctccatcaa cgcggacaac 1700  
 ggccacctgt tcgccctcag gtctctggac tacgaggccc tgcagggggt 1750  
 ccagttccgc gtgggcgctt cagaccacgg ctccccggcg ctgagcagcg 1800  
 aggcgctggt gcgcgtggtg gtgctggacg ccaacgacaa ctcgcccttc 1850  
 gtgctgtacc cgctgcagaa cggtcccgcg ccctgcaccg agctggtgcc 1900  
 ccgggcgggc gagccgggct acctggtgac caagggtggtg gcggtggacg 1950  
 gcgactcggg ccagaacgcc tggctgtcgt accagctgct caaggccacg 2000  
 gagctcggtc tgttcggcgt gtgggcgcac aatggcgagg tgcgcaccgc 2050  
 caggctgctg agcgagcgcg acgcggccaa gcacaggctg gtggtgctgg 2100  
 tcaaggacaa tggcgagcct ccgcgctcgg ccaccgccac gctgcacgtg 2150  
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 cccgaccag gccaggccg acttgctcac cgtctacctg gtggtggcgt 2250  
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 gtgcggtgtg gtaggaggag cagggcggcc tcggtgggtc gctgcttggg 2350  
 gcccgagggc cccttccag ggcattctgt ggacatgagc ggcaccagga 2400  
 ccctatccca gagctaccag tatgaggtgt gtctggcagg aggctcaggg 2450  
 accaatgagt tcaagttcct gaagccgatt atccccaact tccctcccca 2500  
 gtgccctggg aaagaaatac aaggaaattc taccttcccc aataactttg 2550  
 ggttcaatat tcagtgaaca tagttgactt ttacattcca taggtatttt 2600

attttgtggc atttccatgc caatgtttat ttcccccaat ttgtgtgtat 2650  
gtaatatgtt acggattttac tcttgatttt tctcatgttc tttctccctt 2700  
tgtttttaaag tgaacattta cctttattcc tggttctt 2738

<210> 405  
<211> 798  
<212> PRT  
<213> Homo sapiens

<400> 405  
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Phe Ser Phe Leu Leu Leu Gly Leu Ser Leu Ala Gly Ala Ala Glu  
20 25 30  
Pro Arg Ser Tyr Ser Val Val Glu Glu Thr Glu Gly Ser Ser Phe  
35 40 45  
Val Thr Asn Leu Ala Lys Asp Leu Gly Leu Glu Gln Arg Glu Phe  
50 55 60  
Ser Arg Arg Gly Val Arg Val Val Ser Arg Gly Asn Lys Leu His  
65 70 75  
Leu Gln Leu Asn Gln Glu Thr Ala Asp Leu Leu Leu Asn Glu Lys  
80 85 90  
Leu Asp Arg Glu Asp Leu Cys Gly His Thr Glu Pro Cys Val Leu  
95 100 105  
Arg Phe Gln Val Leu Leu Glu Ser Pro Phe Glu Phe Phe Gln Ala  
110 115 120  
Glu Leu Gln Val Ile Asp Ile Asn Asp His Ser Pro Val Phe Leu  
125 130 135  
Asp Lys Gln Met Leu Val Lys Val Ser Glu Ser Ser Pro Pro Gly  
140 145 150  
Thr Thr Phe Pro Leu Lys Asn Ala Glu Asp Leu Asp Val Gly Gln  
155 160 165  
Asn Asn Ile Glu Asn Tyr Ile Ile Ser Pro Asn Ser Tyr Phe Arg  
170 175 180  
Val Leu Thr Arg Lys Arg Ser Asp Gly Arg Lys Tyr Pro Glu Leu  
185 190 195  
Val Leu Asp Lys Ala Leu Asp Arg Glu Glu Glu Ala Glu Leu Arg  
200 205 210  
Leu Thr Leu Thr Ala Leu Asp Gly Gly Ser Pro Pro Arg Ser Gly  
215 220 225  
Thr Ala Gln Val Tyr Ile Glu Val Leu Asp Val Asn Asp Asn Ala

	230	235	240
Pro Glu Phe Glu	Gln Pro Phe Tyr Arg	Val Gln Ile Ser Glu	Asp
	245	250	255
Ser Pro Val Gly	Phe Leu Val Val Lys	Val Ser Ala Thr Asp	Val
	260	265	270
Asp Thr Gly Val	Asn Gly Glu Ile Ser	Tyr Ser Leu Phe Gln	Ala
	275	280	285
Ser Glu Glu Ile	Gly Lys Thr Phe Lys	Ile Asn Pro Leu Thr	Gly
	290	295	300
Glu Ile Glu Leu	Lys Lys Gln Leu Asp	Phe Glu Lys Leu Gln	Ser
	305	310	315
Tyr Glu Val Asn	Ile Glu Ala Arg Asp	Ala Gly Thr Phe Ser	Gly
	320	325	330
Lys Cys Thr Val	Leu Ile Gln Val Ile	Asp Val Asn Asp His	Ala
	335	340	345
Pro Glu Val Thr	Met Ser Ala Phe Thr	Ser Pro Ile Pro Glu	Asn
	350	355	360
Ala Pro Glu Thr	Val Val Ala Leu Phe	Ser Val Ser Asp Leu	Asp
	365	370	375
Ser Gly Glu Asn	Gly Lys Ile Ser Cys	Ser Ile Gln Glu Asp	Leu
	380	385	390
Pro Phe Leu Leu	Lys Ser Ala Glu Asn	Phe Tyr Thr Leu Leu	Thr
	395	400	405
Glu Arg Pro Leu	Asp Arg Glu Ser Arg	Ala Glu Tyr Asn Ile	Thr
	410	415	420
Ile Thr Val Thr	Asp Leu Gly Thr Pro	Met Leu Ile Thr Gln	Leu
	425	430	435
Asn Met Thr Val	Leu Ile Ala Asp Val	Asn Asp Asn Ala Pro	Ala
	440	445	450
Phe Thr Gln Thr	Ser Tyr Thr Leu Phe	Val Arg Glu Asn Asn	Ser
	455	460	465
Pro Ala Leu His	Ile Arg Ser Val Ser	Ala Thr Asp Arg Asp	Ser
	470	475	480
Gly Thr Asn Ala	Gln Val Thr Tyr Ser	Leu Leu Pro Pro Gln	Asp
	485	490	495
Pro His Leu Pro	Leu Thr Ser Leu Val	Ser Ile Asn Ala Asp	Asn
	500	505	510
Gly His Leu Phe	Ala Leu Arg Ser Leu	Asp Tyr Glu Ala Leu	Gln
	515	520	525



Gly Phe Gln Phe Arg Val Gly Ala Ser Asp His Gly Ser Pro Ala	530	535	540
Leu Ser Ser Glu Ala Leu Val Arg Val Val Val Leu Asp Ala Asn	545	550	555
Asp Asn Ser Pro Phe Val Leu Tyr Pro Leu Gln Asn Gly Ser Ala	560	565	570
Pro Cys Thr Glu Leu Val Pro Arg Ala Ala Glu Pro Gly Tyr Leu	575	580	585
Val Thr Lys Val Val Ala Val Asp Gly Asp Ser Gly Gln Asn Ala	590	595	600
Trp Leu Ser Tyr Gln Leu Leu Lys Ala Thr Glu Leu Gly Leu Phe	605	610	615
Gly Val Trp Ala His Asn Gly Glu Val Arg Thr Ala Arg Leu Leu	620	625	630
Ser Glu Arg Asp Ala Ala Lys His Arg Leu Val Val Leu Val Lys	635	640	645
Asp Asn Gly Glu Pro Pro Arg Ser Ala Thr Ala Thr Leu His Val	650	655	660
Leu Leu Val Asp Gly Phe Ser Gln Pro Tyr Leu Pro Leu Pro Glu	665	670	675
Ala Ala Pro Thr Gln Ala Gln Ala Asp Leu Leu Thr Val Tyr Leu	680	685	690
Val Val Ala Leu Ala Ser Val Ser Ser Leu Phe Leu Phe Ser Val	695	700	705
Leu Leu Phe Val Ala Val Arg Leu Cys Arg Arg Ser Arg Ala Ala	710	715	720
Ser Val Gly Arg Cys Leu Val Pro Glu Gly Pro Leu Pro Gly His	725	730	735
Leu Val Asp Met Ser Gly Thr Arg Thr Leu Ser Gln Ser Tyr Gln	740	745	750
Tyr Glu Val Cys Leu Ala Gly Gly Ser Gly Thr Asn Glu Phe Lys	755	760	765
Phe Leu Lys Pro Ile Ile Pro Asn Phe Pro Pro Gln Cys Pro Gly	770	775	780
Lys Glu Ile Gln Gly Asn Ser Thr Phe Pro Asn Asn Phe Gly Phe	785	790	795
Asn Ile Gln			

<210> 406

<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 406  
ctgagaacgc gcctgaaact gtg 23

<210> 407  
<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 407  
agcgttgtca ttgacatcgg cg 22

<210> 408  
<211> 50  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 408  
ttagttgctc cattcaggag gatctaccct tcctcctgaa atccgcggaa 50

<210> 409  
<211> 1379  
<212> DNA  
<213> Homo sapiens

<400> 409  
accacgcgt ccgcccacgc gtcgcccac gcgtccgccc acgcgtccgc 50  
gcgtagccgt gcgccgattg cctctcggcc tgggcaatgg tcccggctgc 100  
cggtcgacga ccgccccgcg tcatgcggct cctcggctgg tggcaagtat 150  
tgctgtgggt gctgggactt cccgtccgcg gcgtggaggt tgcagaggaa 200  
agtggtcgct tatggtcaga ggagcagcct gctcaccctc tccagggtggg 250  
ggctgtgtac ctgggtgagg aggagctcct gcatgaccgc atggggccagg 300  
acagggcagc agaagaggcc aatgcggtgc tggggctgga cacccaaggc 350  
gatcacatgg tgatgctgtc tgtgattcct ggggaagctg aggacaaagt 400  
gagttcagag cctagcggcg tcacctgtgg tgctggagga gcggaggact 450  
caagggtcaa cgtccgagag agccttttct ctctggatgg cgctggagca 500



80										85					90				
Met	Val	Met	Leu	Ser	Val	Ile	Pro	Gly	Glu	Ala	Glu	Asp	Lys	Val					
				95					100					105					
Ser	Ser	Glu	Pro	Ser	Gly	Val	Thr	Cys	Gly	Ala	Gly	Gly	Ala	Glu					
				110					115					120					
Asp	Ser	Arg	Cys	Asn	Val	Arg	Glu	Ser	Leu	Phe	Ser	Leu	Asp	Gly					
				125					130					135					
Ala	Gly	Ala	His	Phe	Pro	Asp	Arg	Glu	Glu	Glu	Tyr	Tyr	Thr	Glu					
				140					145					150					
Pro	Glu	Val	Ala	Glu	Ser	Asp	Ala	Ala	Pro	Thr	Glu	Asp	Ser	Asn					
				155					160					165					
Asn	Thr	Glu	Ser	Leu	Lys	Ser	Pro	Lys	Val	Asn	Cys	Glu	Glu	Arg					
				170					175					180					
Asn	Ile	Thr	Gly	Leu	Glu	Asn	Phe	Thr	Leu	Lys	Ile	Leu	Asn	Met					
				185					190					195					
Ser	Gln	Asp	Leu	Met	Asp	Phe	Leu	Asn	Pro	Asn	Gly	Ser	Asp	Cys					
				200					205					210					
Thr	Leu	Val	Leu	Phe	Tyr	Thr	Pro	Trp	Cys	Arg	Phe	Ser	Ala	Ser					
				215					220					225					
Leu	Ala	Pro	His	Phe	Asn	Ser	Leu	Pro	Arg	Ala	Phe	Pro	Ala	Leu					
				230					235					240					
His	Phe	Leu	Ala	Leu	Asp	Ala	Ser	Gln	His	Ser	Ser	Leu	Ser	Thr					
				245					250					255					
Arg	Phe	Gly	Thr	Val	Ala	Val	Pro	Asn	Ile	Leu	Leu	Phe	Gln	Gly					
				260					265					270					
Ala	Lys	Pro	Met	Ala	Arg	Phe	Asn	His	Thr	Asp	Arg	Thr	Leu	Glu					
				275					280					285					
Thr	Leu	Lys	Ile	Phe	Ile	Phe	Asn	Gln	Thr	Gly	Ile	Glu	Ala	Lys					
				290					295					300					
Lys	Asn	Val	Val	Val	Thr	Gln	Ala	Asp	Gln	Ile	Gly	Pro	Leu	Pro					
				305					310					315					
Ser	Thr	Leu	Ile	Lys	Ser	Val	Asp	Trp	Leu	Leu	Val	Phe	Ser	Leu					
				320					325					330					
Phe	Phe	Leu	Ile	Ser	Phe	Ile	Met	Tyr	Ala	Thr	Ile	Arg	Thr	Glu					
				335					340					345					
Ser	Ile	Arg	Trp	Leu	Ile	Pro	Gly	Gln	Glu	Gln	Glu	His	Val	Glu					
				350					355					360					

<210> 411  
<211> 24

<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 411  
cacagagcca gaagtggcgg aatc 24

<210> 412  
<211> 25  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 412  
ccacatgttc ctgctcttgc cctgg 25

<210> 413  
<211> 45  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 413  
cggtagtgc tgtactctag tcctgtttta caccctgtgg tgccg 45

<210> 414  
<211> 1196  
<212> DNA  
<213> Homo sapiens

<400> 414  
cccggctccg ctccctctgc cccctcgggg tcgcgcgccc acgatgctgc 50  
agggccctgg ctcgctgctg ctgctcttcc tcgcctcgca ctgctgcctg 100  
ggctcggcgc gcgggctctt cctctttggc cagcccgaact tctcctacaa 150  
gcgcagcaat tgcaagccca tcccgggtcaa cctgcagctg tgccacggca 200  
tcgaatacca gaacatgcgg ctgcccacc tgctgggcca cgagaccatg 250  
aaggaggtgc tggagcaggc cggcgcttgg atcccgctgg tcatgaagca 300  
gtgccacccg gacaccaaga agttcctgtg ctcgctcttc gccccgtct 350  
gcctcgatga cctagacgag accatccagc catgccactc gctctgcgtg 400  
caggtgaagg accgctgcgc cccggtcatg tccgccttcg gcttcccctg 450  
gcccgaacatg cttgagtgcg accgtttccc ccaggacaac gacctttgca 500  
tccccctcgc tagcagcgac cacctcctgc cagccaccga ggaagctcca 550

aagggtatgtg aagcctgcaa aaataaaaat gatgatgaca acgacataat 600  
 ggaaacgctt tgtaaaaatg attttgact gaaaataaaa gtgaaggaga 650  
 taacctacat caaccgagat accaaaatca tcctggagac caagagcaag 700  
 accatttaca agctgaacgg tgtgtccgaa agggacctga agaaatcggg 750  
 gctgtgggctc aaagacagct tgcagtgcac ctgtgaggag atgaacgaca 800  
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 ctccgcagc atccgcaagc tgcagtgcta gtcccgcat cctgatggct 950  
 ccgacaggcc tgctccagag cagggtgac catttctgct ccgggatctc 1000  
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 agcttcccc tgcttttgc acgtttgcat cccagcatt tcctgagtta 1100  
 taaggccaca ggagtggata gctgttttca cctaaaggaa aagcccaccc 1150  
 gaatcttgta gaaatattca aactaataaa atcatgaata ttttaa 1196

<210> 415

<211> 295

<212> PRT

<213> Homo sapiens

<400> 415

Met	Leu	Gln	Gly	Pro	Gly	Ser	Leu	Leu	Leu	Leu	Phe	Leu	Ala	Ser
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His	Cys	Cys	Leu	Gly	Ser	Ala	Arg	Gly	Leu	Phe	Leu	Phe	Gly	Gln
				20					25					30

Pro	Asp	Phe	Ser	Tyr	Lys	Arg	Ser	Asn	Cys	Lys	Pro	Ile	Pro	Val
				35					40					45

Asn	Leu	Gln	Leu	Cys	His	Gly	Ile	Glu	Tyr	Gln	Asn	Met	Arg	Leu
				50					55					60

Pro	Asn	Leu	Leu	Gly	His	Glu	Thr	Met	Lys	Glu	Val	Leu	Glu	Gln
				65					70					75

Ala	Gly	Ala	Trp	Ile	Pro	Leu	Val	Met	Lys	Gln	Cys	His	Pro	Asp
				80					85					90

Thr	Lys	Lys	Phe	Leu	Cys	Ser	Leu	Phe	Ala	Pro	Val	Cys	Leu	Asp
				95					100					105

Asp	Leu	Asp	Glu	Thr	Ile	Gln	Pro	Cys	His	Ser	Leu	Cys	Val	Gln
				110					115					120

Val	Lys	Asp	Arg	Cys	Ala	Pro	Val	Met	Ser	Ala	Phe	Gly	Phe	Pro
				125					130					135

Trp	Pro	Asp	Met	Leu	Glu	Cys	Asp	Arg	Phe	Pro	Gln	Asp	Asn	Asp	
				140					145					150	
Leu	Cys	Ile	Pro	Leu	Ala	Ser	Ser	Asp	His	Leu	Leu	Pro	Ala	Thr	
				155					160					165	
Glu	Glu	Ala	Pro	Lys	Val	Cys	Glu	Ala	Cys	Lys	Asn	Lys	Asn	Asp	
				170					175					180	
Asp	Asp	Asn	Asp	Ile	Met	Glu	Thr	Leu	Cys	Lys	Asn	Asp	Phe	Ala	
				185					190					195	
Leu	Lys	Ile	Lys	Val	Lys	Glu	Ile	Thr	Tyr	Ile	Asn	Arg	Asp	Thr	
				200					205					210	
Lys	Ile	Ile	Leu	Glu	Thr	Lys	Ser	Lys	Thr	Ile	Tyr	Lys	Leu	Asn	
				215					220					225	
Gly	Val	Ser	Glu	Arg	Asp	Leu	Lys	Lys	Ser	Val	Leu	Trp	Leu	Lys	
				230					235					240	
Asp	Ser	Leu	Gln	Cys	Thr	Cys	Glu	Glu	Met	Asn	Asp	Ile	Asn	Ala	
				245					250					255	
Pro	Tyr	Leu	Val	Met	Gly	Gln	Lys	Gln	Gly	Gly	Glu	Leu	Val	Ile	
				260					265					270	
Thr	Ser	Val	Lys	Arg	Trp	Gln	Lys	Gly	Gln	Arg	Glu	Phe	Lys	Arg	
				275					280					285	
Ile	Ser	Arg	Ser	Ile	Arg	Lys	Leu	Gln	Cys						
				290					295						

<210> 416

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 416

cctggctcgc tgctgctgct c 21

<210> 417

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 417

cctcacaggt gcactgcaag ctgtc 25

<210> 418

<211> 47

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 418

ctcttctctt ttggccagcc cgacttctcc tacaagcgca gaattgc 47

<210> 419

<211> 1830

<212> DNA

<213> Homo sapiens

<400> 419

gtggaggccg ccgacgatgg cggggccgac ggaggccgag acggggttgg 50  
ccgagccccg ggccctgtgc gcgcagcggg gccaccgcac ctacgcgcgc 100  
cgctgggtgt tctgtctcgc gatcagcctg ctcaactgct ccaacgccac 150  
gctgtggctc agctttgcac ctgtggctga cgtcattgct gaggacttgg 200  
tctgtccat ggagcagatc aactggctgt cactggtcta cctcgtggta 250  
tccaccccat ttggcgtggc ggccatctgg atcctggact ccgtcgggct 300  
ccgtgcggcg accatcctgg gtgcgtggct gaactttgcc gggagtgtgc 350  
tacgcatggg gccctgcatg gttgttggga cccaaaacc atttgccttc 400  
ctcatgggtg gccagagcct ctgtgccctt gccagagcc tggatcatctt 450  
ctctccagcc aagctggctg ccttgtgggt cccagagcac cagcgagcca 500  
cggccaacat gctcgccacc atgtogaacc ctctgggcgt ccttgtggcc 550  
aatgtgctgt cccctgtgct ggtcaagaag ggtgaggaca ttccgttaat 600  
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Gly	Thr	Gln	Asn	Pro 125	Phe	Ala	Phe	Leu	Met 130	Gly	Gly	Gln	Ser	Leu 135
Cys	Ala	Leu	Ala	Gln 140	Ser	Leu	Val	Ile	Phe 145	Ser	Pro	Ala	Lys	Leu 150
Ala	Ala	Leu	Trp	Phe 155	Pro	Glu	His	Gln	Arg 160	Ala	Thr	Ala	Asn	Met 165
Leu	Ala	Thr	Met	Ser 170	Asn	Pro	Leu	Gly	Val 175	Leu	Val	Ala	Asn	Val 180
Leu	Ser	Pro	Val	Leu 185	Val	Lys	Lys	Gly	Glu 190	Asp	Ile	Pro	Leu	Met 195
Leu	Gly	Val	Tyr	Thr 200	Ile	Pro	Ala	Gly	Val 205	Val	Cys	Leu	Leu	Ser 210
Thr	Ile	Cys	Leu	Trp 215	Glu	Ser	Val	Pro	Pro 220	Thr	Pro	Pro	Ser	Ala 225
Gly	Ala	Ala	Ser	Ser 230	Thr	Ser	Glu	Lys	Phe 235	Leu	Asp	Gly	Leu	Lys 240
Leu	Gln	Leu	Met	Trp 245	Asn	Lys	Ala	Tyr	Val 250	Ile	Leu	Ala	Val	Cys 255
Leu	Gly	Gly	Met	Ile 260	Gly	Ile	Ser	Ala	Ser 265	Phe	Ser	Ala	Leu	Leu 270
Glu	Gln	Ile	Leu	Cys 275	Ala	Ser	Gly	His	Ser 280	Ser	Gly	Phe	Ser	Gly 285
Leu	Cys	Gly	Ala	Leu 290	Phe	Ile	Thr	Phe	Gly 295	Ile	Leu	Gly	Ala	Leu 300
Ala	Leu	Gly	Pro	Tyr 305	Val	Asp	Arg	Thr	Lys 310	His	Phe	Thr	Glu	Ala 315
Thr	Lys	Ile	Gly	Leu 320	Cys	Leu	Phe	Ser	Leu 325	Ala	Cys	Val	Pro	Phe 330
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Thr	Cys	Ser	Leu	Leu 350	Gly	Leu	Phe	Gly	Phe 355	Ser	Val	Gly	Pro	Val 360
Ala	Met	Glu	Leu	Ala 365	Val	Glu	Cys	Ser	Phe 370	Pro	Val	Gly	Glu	Gly 375
Ala	Ala	Thr	Gly	Met 380	Ile	Phe	Val	Leu	Gly 385	Gln	Ala	Glu	Gly	Ile 390
Leu	Ile	Met	Leu	Ala 395	Met	Thr	Ala	Leu	Thr 400	Val	Arg	Arg	Ser	Glu 405

Pro Ser Leu Ser Thr Cys Gln Gln Gly Glu Asp Pro Leu Asp Trp  
410 415 420

Thr Val Ser Leu Leu Leu Met Ala Gly Leu Cys Thr Phe Phe Ser  
425 430 435

Cys Ile Leu Ala Val Phe Phe His Thr Pro Tyr Arg Arg Leu Gln  
440 445 450

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455 460 465

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Gly Val Leu Gly Pro Ser Thr Ala Thr Pro Glu Cys Thr Ala Arg  
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Gly Ala Ser Leu Glu Asp Pro Arg Gly Pro Gly Ser Pro His Pro  
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Ala Cys His Arg Ala Thr Pro Arg Ala Gln Gly Pro Ala Ala Thr  
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Asp Ala Pro Ser Arg Pro Gly Arg Leu Ala Gly Arg Val Gln Ala  
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<210> 424

<211> 4313

<212> DNA

<213> Homo sapiens

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 <211> 1184  
 <212> PRT  
 <213> Homo sapiens

<400> 425  
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 Thr Val Lys Tyr Gln Val Ser Glu Glu Val Pro Ser Gly Thr Val  
 35 40 45  
 Ile Gly Lys Leu Ser Gln Glu Leu Gly Arg Glu Glu Arg Arg Arg  
 50 55 60  
 Gln Ala Gly Ala Ala Phe Gln Val Leu Gln Leu Pro Gln Ala Leu  
 65 70 75  
 Pro Ile Gln Val Asp Ser Glu Glu Gly Leu Leu Ser Thr Gly Arg  
 80 85 90  
 Arg Leu Asp Arg Glu Gln Leu Cys Arg Gln Trp Asp Pro Cys Leu  
 95 100 105  
 Val Ser Phe Asp Val Leu Ala Thr Gly Asp Leu Ala Leu Ile His  
 110 115 120  
 Val Glu Ile Gln Val Leu Asp Ile Asn Asp His Gln Pro Arg Phe  
 125 130 135  
 Pro Lys Gly Glu Gln Glu Leu Glu Ile Ser Glu Ser Ala Ser Leu  
 140 145 150  
 Arg Thr Arg Ile Pro Leu Asp Arg Ala Leu Asp Pro Asp Thr Gly  
 155 160 165  
 Pro Asn Thr Leu His Thr Tyr Thr Leu Ser Pro Ser Glu His Phe  
 170 175 180  
 Ala Leu Asp Val Ile Val Gly Pro Asp Glu Thr Lys His Ala Glu  
 185 190 195

Leu Ile Val Val	Lys Glu Leu Asp Arg	Glu Ile His Ser Phe	Phe
200	205		210
Asp Leu Val Leu	Thr Ala Tyr Asp Asn	Gly Asn Pro Pro Lys	Ser
215	220		225
Gly Thr Ser Leu	Val Lys Val Asn Val	Leu Asp Ser Asn Asp	Asn
230	235		240
Ser Pro Ala Phe	Ala Glu Ser Ser Leu	Ala Leu Glu Ile Gln	Glu
245	250		255
Asp Ala Ala Pro	Gly Thr Leu Leu Ile	Lys Leu Thr Ala Thr	Asp
260	265		270
Pro Asp Gln Gly	Pro Asn Gly Glu Val	Glu Phe Phe Leu Ser	Lys
275	280		285
His Met Pro Pro	Glu Val Leu Asp Thr	Phe Ser Ile Asp Ala	Lys
290	295		300
Thr Gly Gln Val	Ile Leu Arg Arg Pro	Leu Asp Tyr Glu Lys	Asn
305	310		315
Pro Ala Tyr Glu	Val Asp Val Gln Ala	Arg Asp Leu Gly Pro	Asn
320	325		330
Pro Ile Pro Ala	His Cys Lys Val Leu	Ile Lys Val Leu Asp	Val
335	340		345
Asn Asp Asn Ile	Pro Ser Ile His Val	Thr Trp Ala Ser Gln	Pro
350	355		360
Ser Leu Val Ser	Glu Ala Leu Pro Lys	Asp Ser Phe Ile Ala	Leu
365	370		375
Val Met Ala Asp	Asp Leu Asp Ser Gly	His Asn Gly Leu Val	His
380	385		390
Cys Trp Leu Ser	Gln Glu Leu Gly His	Phe Arg Leu Lys Arg	Thr
395	400		405
Asn Gly Asn Thr	Tyr Met Leu Leu Thr	Asn Ala Thr Leu Asp	Arg
410	415		420
Glu Gln Trp Pro	Lys Tyr Thr Leu Thr	Leu Leu Ala Gln Asp	Gln
425	430		435
Gly Leu Gln Pro	Leu Ser Ala Lys Lys	Gln Leu Ser Ile Gln	Ile
440	445		450
Ser Asp Ile Asn	Asp Asn Ala Pro Val	Phe Glu Lys Ser Arg	Tyr
455	460		465
Glu Val Ser Thr	Arg Glu Asn Asn Leu	Pro Ser Leu His Leu	Ile
470	475		480
Thr Ile Lys Ala	His Asp Ala Asp Leu	Gly Ile Asn Gly Lys	Val



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Asp	Ser	Asn	Thr	Gly	Glu	Val	Thr	Ala	Gln	Arg	Ser	Leu	Asn	Tyr					
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Glu	Glu	Met	Ala	Gly	Phe	Glu	Phe	Gln	Val	Ile	Ala	Glu	Asp	Ser					
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Gly	Gln	Pro	Met	Leu	Ala	Ser	Ser	Val	Ser	Val	Trp	Val	Ser	Leu					
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Leu	Asp	Ala	Asn	Asp	Asn	Ala	Pro	Glu	Val	Val	Gln	Pro	Val	Leu					
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Ser	Asp	Gly	Lys	Ala	Ser	Leu	Ser	Val	Leu	Val	Asn	Ala	Ser	Thr					
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Gly	His	Leu	Leu	Val	Pro	Ile	Glu	Thr	Pro	Asn	Gly	Leu	Gly	Pro					
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Phe	Leu	Leu	Thr	Thr	Ile	Val	Ala	Arg	Asp	Ala	Asp	Ser	Gly	Ala					
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Asn	Gly	Glu	Pro	Leu	Tyr	Ser	Ile	Arg	Asn	Gly	Asn	Glu	Ala	His					
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Leu	Phe	Ile	Leu	Asn	Pro	His	Thr	Gly	Gln	Leu	Phe	Val	Asn	Val					
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Thr	Asn	Ala	Ser	Ser	Leu	Ile	Gly	Ser	Glu	Trp	Glu	Leu	Glu	Ile					
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Val	Val	Glu	Asp	Gln	Gly	Ser	Pro	Pro	Leu	Gln	Thr	Arg	Ala	Leu					
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Leu	Arg	Val	Met	Phe	Val	Thr	Ser	Val	Asp	His	Leu	Arg	Asp	Ser					
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Ala	Arg	Lys	Pro	Gly	Ala	Leu	Ser	Met	Ser	Met	Leu	Thr	Val	Ile					
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Cys	Leu	Ala	Val	Leu	Leu	Gly	Ile	Phe	Gly	Leu	Ile	Leu	Ala	Leu					
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Phe	Met	Ser	Ile	Cys	Arg	Thr	Glu	Lys	Lys	Asp	Asn	Arg	Ala	Tyr					
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Asn	Cys	Arg	Glu	Ala	Glu	Ser	Thr	Tyr	Arg	Gln	Gln	Pro	Lys	Arg					
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Pro	Gln	Lys	His	Ile	Gln	Lys	Ala	Asp	Ile	His	Leu	Val	Pro	Val					
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785	790		795
Lys Asp Val Asp	Lys Glu Ala Met Met	Glu Ala Gly Trp Asp	Pro
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Cys Leu Gln Ala	Pro Phe His Leu Thr	Pro Thr Leu Tyr Arg	Thr
815	820		825
Leu Arg Asn Gln	Gly Asn Gln Gly Ala	Pro Ala Glu Ser Arg	Glu
830	835		840
Val Leu Gln Asp	Thr Val Asn Leu Leu	Phe Asn His Pro Arg	Gln
845	850		855
Arg Asn Ala Ser	Arg Glu Asn Leu Asn	Leu Pro Glu Pro Gln	Pro
860	865		870
Ala Thr Gly Gln	Pro Arg Ser Arg Pro	Leu Lys Val Ala Gly	Ser
875	880		885
Pro Thr Gly Arg	Leu Ala Gly Asp Gln	Gly Ser Glu Glu Ala	Pro
890	895		900
Gln Arg Pro Pro	Ala Ser Ser Ala Thr	Leu Arg Arg Gln Arg	His
905	910		915
Leu Asn Gly Lys	Val Ser Pro Glu Lys	Glu Ser Gly Pro Arg	Gln
920	925		930
Ile Leu Arg Ser	Leu Val Arg Leu Ser	Val Ala Ala Phe Ala	Glu
935	940		945
Arg Asn Pro Val	Glu Glu Leu Thr Val	Asp Ser Pro Pro Val	Gln
950	955		960
Gln Ile Ser Gln	Leu Leu Ser Leu Leu	His Gln Gly Gln Phe	Gln
965	970		975
Pro Lys Pro Asn	His Arg Gly Asn Lys	Tyr Leu Ala Lys Pro	Gly
980	985		990
Gly Ser Arg Ser	Ala Ile Pro Asp Thr	Asp Gly Pro Ser Ala	Arg
995	1000		1005
Ala Gly Gly Gln	Thr Asp Pro Glu Gln	Glu Glu Gly Pro Leu	Asp
1010	1015		1020
Pro Glu Glu Asp	Leu Ser Val Lys Gln	Leu Leu Glu Glu Glu	Leu
1025	1030		1035
Ser Ser Leu Leu	Asp Pro Ser Thr Gly	Leu Ala Leu Asp Arg	Leu
1040	1045		1050
Ser Ala Pro Asp	Pro Ala Trp Met Ala	Arg Leu Ser Leu Pro	Leu
1055	1060		1065
Thr Thr Asn Tyr	Arg Asp Asn Val Ile	Ser Pro Asp Ala Ala	Ala

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Ser Glu Met Ser Ser Leu Leu Glu Met Leu Leu Glu Gln Arg Ser		
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Ser Met Pro Val Glu Ala Ala Ser Glu Ala Leu Arg Arg Leu Ser		
1130	1135	1140
Val Cys Gly Arg Thr Leu Ser Leu Asp Leu Ala Thr Ser Ala Ala		
1145	1150	1155
Ser Gly Met Lys Val Gln Gly Asp Pro Gly Gly Lys Thr Gly Thr		
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<210> 427  
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 <212> DNA  
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<220>  
 <223> Synthetic oligonucleotide probe

<400> 427  
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 <212> DNA  
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<220>  
 <223> Synthetic oligonucleotide probe

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<210> 429  
 <211> 2037

<212> DNA  
<213> Homo sapiens

<400> 429

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<210> 430

<211> 455

<212> PRT

<213> Homo sapiens

<400> 430

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			20						25					30
Lys	Asp	Tyr	Glu	Ile	Arg	Gln	Tyr	Val	Val	Gln	Val	Ile	Phe	Ser
			35						40					45
Val	Thr	Phe	Ala	Phe	Ser	Cys	Thr	Met	Phe	Glu	Leu	Ile	Ile	Phe
			50						55					60
Glu	Ile	Leu	Gly	Val	Leu	Asn	Ser	Ser	Ser	Arg	Tyr	Phe	His	Trp
			65						70					75
Lys	Met	Asn	Leu	Cys	Val	Ile	Leu	Leu	Ile	Leu	Val	Phe	Met	Val
			80						85					90
Pro	Phe	Tyr	Ile	Gly	Tyr	Phe	Ile	Val	Ser	Asn	Ile	Arg	Leu	Leu
			95						100					105
His	Lys	Gln	Arg	Leu	Leu	Phe	Ser	Cys	Leu	Leu	Trp	Leu	Thr	Phe
			110						115					120

Met	Tyr	Phe	Phe	Trp	Lys	Leu	Gly	Asp	Pro	Phe	Pro	Ile	Leu	Ser		125	130	135
Pro	Lys	His	Gly	Ile	Leu	Ser	Ile	Glu	Gln	Leu	Ile	Ser	Arg	Val		140	145	150
Gly	Val	Ile	Gly	Val	Thr	Leu	Met	Ala	Leu	Leu	Ser	Gly	Phe	Gly		155	160	165
Ala	Val	Asn	Cys	Pro	Tyr	Thr	Tyr	Met	Ser	Tyr	Phe	Leu	Arg	Asn		170	175	180
Val	Thr	Asp	Thr	Asp	Ile	Leu	Ala	Leu	Glu	Arg	Arg	Leu	Leu	Gln		185	190	195
Thr	Met	Asp	Met	Ile	Ile	Ser	Lys	Lys	Lys	Arg	Met	Ala	Met	Ala		200	205	210
Arg	Arg	Thr	Met	Phe	Gln	Lys	Gly	Glu	Val	His	Asn	Lys	Pro	Ser		215	220	225
Gly	Phe	Trp	Gly	Met	Ile	Lys	Ser	Val	Thr	Thr	Ser	Ala	Ser	Gly		230	235	240
Ser	Glu	Asn	Leu	Thr	Leu	Ile	Gln	Gln	Glu	Val	Asp	Ala	Leu	Glu		245	250	255
Glu	Leu	Ser	Arg	Gln	Leu	Phe	Leu	Glu	Thr	Ala	Asp	Leu	Tyr	Ala		260	265	270
Thr	Lys	Glu	Arg	Ile	Glu	Tyr	Ser	Lys	Thr	Phe	Lys	Gly	Lys	Tyr		275	280	285
Phe	Asn	Phe	Leu	Gly	Tyr	Phe	Phe	Ser	Ile	Tyr	Cys	Val	Trp	Lys		290	295	300
Ile	Phe	Met	Ala	Thr	Ile	Asn	Ile	Val	Phe	Asp	Arg	Val	Gly	Lys		305	310	315
Thr	Asp	Pro	Val	Thr	Arg	Gly	Ile	Glu	Ile	Thr	Val	Asn	Tyr	Leu		320	325	330
Gly	Ile	Gln	Phe	Asp	Val	Lys	Phe	Trp	Ser	Gln	His	Ile	Ser	Phe		335	340	345
Ile	Leu	Val	Gly	Ile	Ile	Ile	Val	Thr	Ser	Ile	Arg	Gly	Leu	Leu		350	355	360
Ile	Thr	Leu	Thr	Lys	Phe	Phe	Tyr	Ala	Ile	Ser	Ser	Ser	Lys	Ser		365	370	375
Ser	Asn	Val	Ile	Val	Leu	Leu	Leu	Ala	Gln	Ile	Met	Gly	Met	Tyr		380	385	390
Phe	Val	Ser	Ser	Val	Leu	Leu	Ile	Arg	Met	Ser	Met	Pro	Leu	Glu		395	400	405
Tyr	Arg	Thr	Ile	Ile	Thr	Glu	Val	Leu	Gly	Glu	Leu	Gln	Phe	Asn				

410	415	420
Phe Tyr His Arg Trp Phe Asp Val Ile	Phe Leu Val Ser Ala Leu	
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Ser Ser Ile Leu Phe Leu Tyr Leu Ala	His Lys Gln Ala Pro Glu	
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Lys Gln Met Ala Pro		
455		

<210> 431  
 <211> 407  
 <212> DNA  
 <213> Homo sapiens  
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 <222> 78, 81, 113, 157, 224, 297  
 <223> unknown base

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 ttgtacnggt gatcttctcc gtgacgtttg ccatttcttg caccatgttt 200  
 gagctcatca tctttgaaat cttnngagta ttgaatagca gctcccgta 250  
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cattttcttg caccatgttt gagctcatca tntttgaaat nttaggagta 250  
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<210> 435  
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<210> 436  
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 ttctcacggg ctgtcgcctt caatctggac gtgatgggtg ccttgcgcaa 150  
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<210> 437  
<211> 1141  
<212> PRT  
<213> Homo sapiens

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Ala Val Ala Phe Asn Leu Asp Val Met Gly Ala Leu Arg Lys Glu  
35 40 45  
Gly Glu Pro Gly Ser Leu Phe Gly Phe Ser Val Ala Leu His Arg  
50 55 60  
Gln Leu Gln Pro Arg Pro Gln Ser Trp Leu Leu Val Gly Ala Pro  
65 70 75  
Gln Ala Leu Ala Leu Pro Gly Gln Gln Ala Asn Arg Thr Gly Gly

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				95					100					105					
Val	Asp	Ile	Asp	Gln	Gly	Ala	Asp	Met	Gln	Lys	Glu	Ser	Lys	Glu					
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Asn	Gln	Trp	Leu	Gly	Val	Ser	Val	Arg	Ser	Gln	Gly	Pro	Gly	Gly					
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Lys	Ile	Val	Thr	Cys	Ala	His	Arg	Tyr	Glu	Ala	Arg	Gln	Arg	Val					
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Asp	Gln	Ile	Leu	Glu	Thr	Arg	Asp	Met	Ile	Gly	Arg	Cys	Phe	Val					
				155					160					165					
Leu	Ser	Gln	Asp	Leu	Ala	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Gly	Glu					
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Trp	Lys	Phe	Cys	Glu	Gly	Arg	Pro	Gln	Gly	His	Glu	Gln	Phe	Gly					
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Phe	Cys	Gln	Gln	Gly	Thr	Ala	Ala	Ala	Phe	Ser	Pro	Asp	Ser	His					
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Tyr	Leu	Leu	Phe	Gly	Ala	Pro	Gly	Thr	Tyr	Asn	Trp	Lys	Gly	Thr					
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Ala	Arg	Val	Glu	Leu	Cys	Ala	Gln	Gly	Ser	Ala	Asp	Leu	Ala	His					
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Leu	Asp	Asp	Gly	Pro	Tyr	Glu	Ala	Gly	Gly	Glu	Lys	Glu	Gln	Asp					
				245					250					255					
Pro	Arg	Leu	Ile	Pro	Val	Pro	Ala	Asn	Ser	Tyr	Phe	Gly	Phe	Ser					
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Ile	Asp	Ser	Gly	Lys	Gly	Leu	Val	Arg	Ala	Glu	Glu	Leu	Ser	Phe					
				275					280					285					
Val	Ala	Gly	Ala	Pro	Arg	Ala	Asn	His	Lys	Gly	Ala	Val	Val	Ile					
				290					295					300					
Leu	Arg	Lys	Asp	Ser	Ala	Ser	Arg	Leu	Val	Pro	Glu	Val	Met	Leu					
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Ser	Gly	Glu	Arg	Leu	Thr	Ser	Gly	Phe	Gly	Tyr	Ser	Leu	Ala	Val					
				320					325					330					
Ala	Asp	Leu	Asn	Ser	Asp	Gly	Trp	Pro	Asp	Leu	Ile	Val	Gly	Ala					
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Pro	Tyr	Phe	Phe	Glu	Arg	Gln	Glu	Glu	Leu	Gly	Gly	Ala	Val	Tyr					
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Val	Tyr	Leu	Asn	Gln	Gly	Gly	His	Trp	Ala	Gly	Ile	Ser	Pro	Leu					
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Arg Leu Cys Gly Ser Pro Asp Ser Met Phe Gly Ile Ser Leu Ala	380	385	390
Val Leu Gly Asp Leu Asn Gln Asp Gly Phe Pro Asp Ile Ala Val	395	400	405
Gly Ala Pro Phe Asp Gly Asp Gly Lys Val Phe Ile Tyr His Gly	410	415	420
Ser Ser Leu Gly Val Val Ala Lys Pro Ser Gln Val Leu Glu Gly	425	430	435
Glu Ala Val Gly Ile Lys Ser Phe Gly Tyr Ser Leu Ser Gly Ser	440	445	450
Leu Asp Met Asp Gly Asn Gln Tyr Pro Asp Leu Leu Val Gly Ser	455	460	465
Leu Ala Asp Thr Ala Val Leu Phe Arg Ala Arg Pro Ile Leu His	470	475	480
Val Ser His Glu Val Ser Ile Ala Pro Arg Ser Ile Asp Leu Glu	485	490	495
Gln Pro Asn Cys Ala Gly Gly His Ser Val Cys Val Asp Leu Arg	500	505	510
Val Cys Phe Ser Tyr Ile Ala Val Pro Ser Ser Tyr Ser Pro Thr	515	520	525
Val Ala Leu Asp Tyr Val Leu Asp Ala Asp Thr Asp Arg Arg Leu	530	535	540
Arg Gly Gln Val Pro Arg Val Thr Phe Leu Ser Arg Asn Leu Glu	545	550	555
Glu Pro Lys His Gln Ala Ser Gly Thr Val Trp Leu Lys His Gln	560	565	570
His Asp Arg Val Cys Gly Asp Ala Met Phe Gln Leu Gln Glu Asn	575	580	585
Val Lys Asp Lys Leu Arg Ala Ile Val Val Thr Leu Ser Tyr Ser	590	595	600
Leu Gln Thr Pro Arg Leu Arg Arg Gln Ala Pro Gly Gln Gly Leu	605	610	615
Pro Pro Val Ala Pro Ile Leu Asn Ala His Gln Pro Ser Thr Gln	620	625	630
Arg Ala Glu Ile His Phe Leu Lys Gln Gly Cys Gly Glu Asp Lys	635	640	645
Ile Cys Gln Ser Asn Leu Gln Leu Val His Ala Arg Phe Cys Thr	650	655	660
Arg Val Ser Asp Thr Glu Phe Gln Pro Leu Pro Met Asp Val Asp			

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Gln	Ala	Asp	Gly	Asp	Asp	Ala	His	Glu	Ala	Gln	Leu	Leu	Val	Met
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Ala	Glu	Lys	Pro	Leu	Cys	Leu	Ser	Asn	Glu	Asn	Ala	Ser	His	Val
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Glu	Cys	Glu	Leu	Gly	Asn	Pro	Met	Lys	Arg	Gly	Ala	Gln	Val	Thr
				755										765
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Ser	Leu	Arg	Thr	Leu	Gly	Ser	Ala	Phe	Leu	Asn	Ile	Met	Trp	Pro
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His	Glu	Ile	Ala	Asn	Gly	Lys	Trp	Leu	Leu	Tyr	Pro	Met	Gln	Val
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Arg	Arg	Arg	Glu	Leu	Glu	Pro	Pro	Glu	Gln	Gln	Glu	Pro	Gly	Glu
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Arg	Gln	Glu	Pro	Ser	Met	Ser	Trp	Trp	Pro	Val	Ser	Ser	Ala	Glu
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Lys	Lys	Lys	Asn	Ile	Thr	Leu	Asp	Cys	Ala	Arg	Gly	Thr	Ala	Asn
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<400> 439  
gctgctgggg actgcaatgt agct 24

<210> 440

<211> 46

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 440

catcctccat gtctcccatg aggtctctat tgctccacga agcatc 46

<210> 441

<211> 1964

<212> DNA

<213> Homo sapiens

<400> 441

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ggagctgcga gcacagtgtc ggctcacaac aagatgtctc aggtgtcagc 150  
cgtactgtgt gtgtgtgcag ccgcttggtg cagtcagtct ctcgcagctg 200  
ccgcggcggt ggctgcagcc ggggggagggt cggacggcgg taattttctg 250  
gatgataaac aatgggtcac cacaatctct cagtatgaca aggaagtcgg 300  
acagtgaac aaattccgag acgaagtaga ggatgattat ttccgcactt 350  
ggagtccagg aaaacccttc gatcaggctt tagatccagc taaggatcca 400  
tgcttaaaga tgaaatgtag tcgccataaa gtatgcattg ctcaagattc 450  
tcagactgca gtctgcatta gtcaccggag gcttacacac aggatgaaag 500  
aagcaggagt agaccatagg cagtggaggg gtcccatatt atccacctgc 550  
aagcagtgcc cagtgggtcta tcccagccct gtttgtgggt cagatgggtca 600  
tacctactct tttcagtgc aactagaata tcaggcatgt gtcttaggaa 650  
aacagatctc agtcaaagt gaaggacatt gccatgtcc ttcagataag 700  
cccaccagta caagcagaaa tgtaagaga gcatgcagtg acctggagtt 750  
cagggaagtg gcaaacagat tgcgggactg gttcaaggcc cttcatgaaa 800  
gtggaagtca aaacaagaag acaaaaacat tgctgaggcc tgagagaagc 850  
agattcgata ccagcatctt gccaatgtgc aaggactcac ttggctggat 900  
gtttaacaga cttgatacaa actatgacct gctattggac cagtcagagc 950



tcagaagcat ttaccttgat aagaatgaac agtgtaccaa ggcattcttc 1000  
aattcttgtg acacatacaa ggacagttta atatctaata atgagtgggtg 1050  
ctactgcttc cagagacagc aagaccacc ttgccagact gagctcagca 1100  
atattcagaa gcggcaaggg gtaaagaagc tcctaggaca gtatatcccc 1150  
ctgtgtgatg aagatgggta ctacaagcca acacaatgtc atggcagtgt 1200  
tggacagtgc tgggtgtgtt acagatatgg aaatgaagtc atgggatcca 1250  
gaataaatgg tgttgcagat tgtgctatag attttgagat ctccggagat 1300  
tttgctagtg gcgattttca tgaatggact gatgatgagg atgatgaaga 1350  
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gggatgatga tgatgggtgg gatgaccatg atgtatacat ttgattgatg 1450  
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cctattttaa attatcttct tccccataa caaatgatt ctaaacctca 1550  
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aaaagaaaat acatatgcag tctagtcaga caaaataaag ttttgaagt 1700  
ctactataat aaatttttca cgagaacaaa ctttgtaa atctccataag 1750  
caaatgaca gctagtgtt gggatcgtac atgttaattt ttgaaagat 1800  
aattctaagt gaaattttaa ataaataaat ttttaatgac ctgggtctta 1850  
aggatttagg aaaaatatgc atgctttaat tgcatttcca aagtagcatc 1900  
ttgctagacc tagatgagtc aggataacag agagatacca catgactcca 1950  
aaaaaaaaaa aaaa 1964

<210> 442  
<211> 436  
<212> PRT  
<213> Homo sapiens

<400> 442  
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Cys Ser Gln Ser Leu Ala Ala Ala Ala Val Ala Ala Ala Gly  
20 25 30  
Gly Arg Ser Asp Gly Gly Asn Phe Leu Asp Asp Lys Gln Trp Leu  
35 40 45  
Thr Thr Ile Ser Gln Tyr Asp Lys Glu Val Gly Gln Trp Asn Lys

10017081-102401

50										55					60				
Phe	Arg	Asp	Glu	Val	Glu	Asp	Asp	Tyr	Phe	Arg	Thr	Trp	Ser	Pro					
				65					70					75					
Gly	Lys	Pro	Phe	Asp	Gln	Ala	Leu	Asp	Pro	Ala	Lys	Asp	Pro	Cys					
				80					85					90					
Leu	Lys	Met	Lys	Cys	Ser	Arg	His	Lys	Val	Cys	Ile	Ala	Gln	Asp					
				95					100					105					
Ser	Gln	Thr	Ala	Val	Cys	Ile	Ser	His	Arg	Arg	Leu	Thr	His	Arg					
				110					115					120					
Met	Lys	Glu	Ala	Gly	Val	Asp	His	Arg	Gln	Trp	Arg	Gly	Pro	Ile					
				125					130					135					
Leu	Ser	Thr	Cys	Lys	Gln	Cys	Pro	Val	Val	Tyr	Pro	Ser	Pro	Val					
				140					145					150					
Cys	Gly	Ser	Asp	Gly	His	Thr	Tyr	Ser	Phe	Gln	Cys	Lys	Leu	Glu					
				155					160					165					
Tyr	Gln	Ala	Cys	Val	Leu	Gly	Lys	Gln	Ile	Ser	Val	Lys	Cys	Glu					
				170					175					180					
Gly	His	Cys	Pro	Cys	Pro	Ser	Asp	Lys	Pro	Thr	Ser	Thr	Ser	Arg					
				185					190					195					
Asn	Val	Lys	Arg	Ala	Cys	Ser	Asp	Leu	Glu	Phe	Arg	Glu	Val	Ala					
				200					205					210					
Asn	Arg	Leu	Arg	Asp	Trp	Phe	Lys	Ala	Leu	His	Glu	Ser	Gly	Ser					
				215					220					225					
Gln	Asn	Lys	Lys	Thr	Lys	Thr	Leu	Leu	Arg	Pro	Glu	Arg	Ser	Arg					
				230					235					240					
Phe	Asp	Thr	Ser	Ile	Leu	Pro	Ile	Cys	Lys	Asp	Ser	Leu	Gly	Trp					
				245					250					255					
Met	Phe	Asn	Arg	Leu	Asp	Thr	Asn	Tyr	Asp	Leu	Leu	Leu	Asp	Gln					
				260					265					270					
Ser	Glu	Leu	Arg	Ser	Ile	Tyr	Leu	Asp	Lys	Asn	Glu	Gln	Cys	Thr					
				275					280					285					
Lys	Ala	Phe	Phe	Asn	Ser	Cys	Asp	Thr	Tyr	Lys	Asp	Ser	Leu	Ile					
				290					295					300					
Ser	Asn	Asn	Glu	Trp	Cys	Tyr	Cys	Phe	Gln	Arg	Gln	Gln	Asp	Pro					
				305					310					315					
Pro	Cys	Gln	Thr	Glu	Leu	Ser	Asn	Ile	Gln	Lys	Arg	Gln	Gly	Val					
				320					325					330					
Lys	Lys	Leu	Leu	Gly	Gln	Tyr	Ile	Pro	Leu	Cys	Asp	Glu	Asp	Gly					
				335					340					345					

Tyr	Tyr	Lys	Pro	Thr	Gln	Cys	His	Gly	Ser	Val	Gly	Gln	Cys	Trp
				350					355					360
Cys	Val	Asp	Arg	Tyr	Gly	Asn	Glu	Val	Met	Gly	Ser	Arg	Ile	Asn
				365					370					375
Gly	Val	Ala	Asp	Cys	Ala	Ile	Asp	Phe	Glu	Ile	Ser	Gly	Asp	Phe
				380					385					390
Ala	Ser	Gly	Asp	Phe	His	Glu	Trp	Thr	Asp	Asp	Glu	Asp	Asp	Glu
				395					400					405
Asp	Asp	Ile	Met	Asn	Asp	Glu	Asp	Glu	Ile	Glu	Asp	Asp	Asp	Glu
				410					415					420
Asp	Glu	Gly	Asp	Asp	Asp	Asp	Gly	Gly	Asp	Asp	His	Asp	Val	Tyr
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<210> 443

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 443

cagcaatatt cagaagcggc aaggg 25

<210> 444

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 444

catcatggtc atcaccacca tcatcatc 28

<210> 445

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 445

ggttactaca agccaacaca atgtcatggc agtggtggac agtgctgg 48

<210> 446

<211> 3617

<212> DNA

<213> Homo sapiens

&lt;400&gt; 446

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 cagggatggg cgacaagatc tggctgcctt tccccgtgct cttcttgcc 150  
 gctctgcctc cgggtgctgct gcctggggcg gccggcttca caccttccct 200  
 cgatagcgac ttcaccttta cccttcccg cggccagaag gagtgtttct 250  
 accagcccat gcccctgaag gcctcgctgg agatcgagta ccaagtttta 300  
 gatggagcag gattagatat tgatttccat cttgcctctc cagaaggcaa 350  
 aaccttagtt ttgaaacaaa gaaaatcaga tggagttcac actgtagaga 400  
 ctgaagttgg tgattacatg ttctgctttg acaatacatt cagcaccatt 450  
 tctgagaagg tgattttctt tgaattaatc ctggataata tgggagaaca 500  
 ggcacaagaa caagaagatt ggaagaaata tattactggc acagatatat 550  
 tggatatgaa actggaagac atcctggaat ccatcaacag catcaagtcc 600  
 agactaagca aaagtgggca catacaaatt ctgcttagag catttgaagc 650  
 tcgtgatcga aacatacaag aaagcaactt tgatagagtc aatttctggt 700  
 ctatggttaa tttagtggtc atggtggtgg tgtcagccat tcaagtttat 750  
 atgctgaaga gtctgtttga agataagagg aaaagtagaa cttaaaactc 800  
 caaactagag tacgtaacat tgaaaaatga ggcataaaaa tgcaataaac 850  
 tgttacagtc aagaccatta atggtcttct ccaaaatatt ttgagatata 900  
 aaagtaggaa acaggtataa ttttaatgtg aaaattaagt cttcactttc 950  
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 attttgcaga atataggttt aactgaatga agccatatta ataactgcat 1050  
 tttcctaact ttgaaaaatt ttgcaaagt cttaggtgat ttaaataaat 1100  
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 cccagaactt ttttgtaa at gcggcagtta caaattaact gtggaagttt 1200  
 tcagttttta gttataaatc acctgagaat tacctaata tggattgaat 1250  
 aaatcttttag actacaaaag cccaactttt ctctatttac atatgcatct 1300  
 ctctataat gtaaatagaa taatagcttt gaaatacaat taggtttttg 1350  
 agatttttat aaccaaatac atttcagtgt aacatattag cagaaagcat 1400  
 tagtctttgt actttgotta cattcccaaa agctgacatt ttcacgattc 1450

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 tctaaccctt aactaaagt taggatttta aaattaaatg tgaggtaaaa 1600  
 taagtttatt tttaatagta tctgtcaagt taatatctgt caacagttaa 1650  
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 attaccagca gttatgaagg aaatattgct aaaatgatct gggcctacca 1750  
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 agaatttaga aaaacttgag aaaaccta ccaaataaa attcacttaa 1850  
 gtagaactat aaataaatat ctagaatctg actggctcat catgacatcc 1900  
 tactcataac ataaatcaaa ggagatgatt aatttccagt tagctggaag 1950  
 aaactttggc tgtaggtttt tattttctac aagaattctg gtttgaatta 2000  
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 tcaagtacta gtaatttaac ttcatcatga atgaactata atttttaagt 2300  
 tatgccatt tataacgttg tttatgacta cattgtgagt tagaaacaaa 2350  
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 ataccctcc cttttgogct gttaaatttg caatgagaag caaatttaca 2700  
 gtaccataac taataaagca gggtagagat ataaactact gcatcttttc 2750  
 tataaaactg tgattaagaa ttctacctct cctgtatggc tgttactgta 2800  
 ctgtactctc tgactoctta cctaacaatg aatttgttac ataattctct 2850  
 acatgtatga tttgtgccac tgatcttaaa cctatgattc agtaacttct 2900

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 cataacccaaa aaagcaaac ttgtaaacag agtaaaaatc tttaatatatt 3050  
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 tccattttcta aattaaagtt atgctaaatt gagtaagctg tttatcactt 3150  
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 atttaactaa ggcccaaccg atttcataa tgtagcagtt accgtgttca 3250  
 cctcacacta aggcttagag tttgctctga tatgcatttg gatgattaat 3300  
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 aaaaaatgag cacttacaat tgtatgtctc ctcaaatgaa gattctttat 3450  
 gtgaaatttt aaaagacatt gattccgcat gtaaggattt ttcatctgaa 3500  
 gtacaataat gcacaatcag tggtgctcaa actgctttat acttataaac 3550  
 agccatotta aataagcaac gtattgtgag tactgatatg tatataataa 3600  
 aaattatcaa aggaaaa 3617

<210> 447

<211> 229

<212> PRT

<213> Homo sapiens

<400> 447

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Ala	Leu	Pro	Pro	Val	Leu	Leu	Pro	Gly	Ala	Ala	Gly	Phe	Thr	Pro
				20					25					30
Ser	Leu	Asp	Ser	Asp	Phe	Thr	Phe	Thr	Leu	Pro	Ala	Gly	Gln	Lys
				35					40					45
Glu	Cys	Phe	Tyr	Gln	Pro	Met	Pro	Leu	Lys	Ala	Ser	Leu	Glu	Ile
				50					55					60
Glu	Tyr	Gln	Val	Leu	Asp	Gly	Ala	Gly	Leu	Asp	Ile	Asp	Phe	His
				65					70					75
Leu	Ala	Ser	Pro	Glu	Gly	Lys	Thr	Leu	Val	Phe	Glu	Gln	Arg	Lys
				80					85					90
Ser	Asp	Gly	Val	His	Thr	Val	Glu	Thr	Glu	Val	Gly	Asp	Tyr	Met
				95					100					105
Phe	Cys	Phe	Asp	Asn	Thr	Phe	Ser	Thr	Ile	Ser	Glu	Lys	Val	Ile

	110		115		120
Phe Phe Glu Leu	Ile Leu Asp Asn Met	Gly Glu Gln Ala Gln Glu			
	125	130			135
Gln Glu Asp Trp	Lys Lys Tyr Ile Thr	Gly Thr Asp Ile Leu Asp			
	140	145			150
Met Lys Leu Glu	Asp Ile Leu Glu Ser	Ile Asn Ser Ile Lys Ser			
	155	160			165
Arg Leu Ser Lys	Ser Gly His Ile Gln	Ile Leu Leu Arg Ala Phe			
	170	175			180
Glu Ala Arg Asp	Arg Asn Ile Gln Glu	Ser Asn Phe Asp Arg Val			
	185	190			195
Asn Phe Trp Ser	Met Val Asn Leu Val	Val Met Val Val Val Ser			
	200	205			210
Ala Ile Gln Val	Tyr Met Leu Lys Ser	Leu Phe Glu Asp Lys Arg			
	215	220			225
Lys Ser Arg Thr					

<210> 448  
 <211> 23  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 448  
 cccagcaggg ctgggagaca aga 23

<210> 449  
 <211> 23  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 449  
 gtcttccagt ttcatatcca ata 23

<210> 450  
 <211> 43  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 450  
 ccagaaggag cacggggaag ggcagccaga tcttgtcgcc cat 43







<400> 454

Met Arg Gly Thr Arg Leu Ala Leu Leu Ala Leu Val Leu Ala Ala  
1 5 10 15

Cys Gly Glu Leu Ala Pro Ala Leu Arg Cys Tyr Val Cys Pro Glu  
20 25 30

Pro Thr Gly Val Ser Asp Cys Val Thr Ile Ala Thr Cys Thr Thr  
35 40 45

Asn Glu Thr Met Cys Lys Thr Thr Leu Tyr Ser Arg Glu Ile Val  
50 55 60

Tyr Pro Phe Gln Gly Asp Ser Thr Val Thr Lys Ser Cys Ala Ser  
65 70 75

Lys Cys Lys Pro Ser Asp Val Asp Gly Ile Gly Gln Thr Leu Pro  
80 85 90

Val Ser Cys Cys Asn Thr Glu Leu Cys Asn Val Asp Gly Ala Pro  
95 100 105

Ala Leu Asn Ser Leu His Cys Gly Ala Leu Thr Leu Leu Pro Leu  
110 115 120

Leu Ser Leu Arg Leu  
125

<210> 455

<211> 1518

<212> DNA

<213> Homo sapiens

<400> 455

ctgcagtcag gactctggga ccgcaggggg ctcccggacc ctgactctgc 50

agccgaaccg gcacggtttc gtggggaccc aggcttgcaa agtgacggtc 100

atTTTctctt tctttctccc tcttgagtcc ttctgagatg atggctctgg 150

gcgcagcggg agctacccgg gtctttgtcg cgatggtagc ggcggtcttc 200

ggcggccacc ctctgctggg agtgagcgcc accttgaact cggttctcaa 250

ttccaacgct atcaagaacc tgccccacc gctgggcggc gctgcggggc 300

accagggctc tgcagtcagc gccgcgccgg gaatcctgta cccggggcggg 350

aataagtacc agaccattga caactaccag ccgtacccgt gcgcagagga 400

cgaggagtgc ggcactgatg agtactgcgc tagtcccacc cgcggagggg 450

acgcagggcgt gcaaattctgt ctgcctgca ggaagcgccg aaaacgctgc 500

atgcgtcacg ctatgtgctg ccccggaat tactgcaaaa atggaatatg 550

tgtgtcttct gatcaaaatc atttcgagg agaaattgag gaaaccatca 600

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 ttatggaact cccctgtgat tgcagtaaata tactgtattg taaattctca 1150  
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 tttcagctta tagttcttaa aagcataacc ctttacccca ttttaattcta 1350  
 gagtctagaa cgcaaggatc tcttggaatg acaaatgata ggtacctaaa 1400  
 atgtaacatg aaaatactag cttattttct gaaatgtact atcttaatgc 1450  
 ttaaattata tttcccttta ggctgtgata gtttttgaaa taaaatttaa 1500  
 catttaaaaa aaaaaaaaa 1518

<210> 456  
 <211> 266  
 <212> PRT  
 <213> Homo sapiens

<400> 456  
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 Met Val Ala Ala Ala Leu Gly Gly His Pro Leu Leu Gly Val Ser  
 20 25 30  
 Ala Thr Leu Asn Ser Val Leu Asn Ser Asn Ala Ile Lys Asn Leu  
 35 40 45  
 Pro Pro Pro Leu Gly Gly Ala Ala Gly His Pro Gly Ser Ala Val  
 50 55 60  
 Ser Ala Ala Pro Gly Ile Leu Tyr Pro Gly Gly Asn Lys Tyr Gln  
 65 70 75

Thr	Ile	Asp	Asn	Tyr	Gln	Pro	Tyr	Pro	Cys	Ala	Glu	Asp	Glu	Glu	
				80					85					90	
Cys	Gly	Thr	Asp	Glu	Tyr	Cys	Ala	Ser	Pro	Thr	Arg	Gly	Gly	Asp	
				95					100					105	
Ala	Gly	Val	Gln	Ile	Cys	Leu	Ala	Cys	Arg	Lys	Arg	Arg	Lys	Arg	
				110					115					120	
Cys	Met	Arg	His	Ala	Met	Cys	Cys	Pro	Gly	Asn	Tyr	Cys	Lys	Asn	
				125					130					135	
Gly	Ile	Cys	Val	Ser	Ser	Asp	Gln	Asn	His	Phe	Arg	Gly	Glu	Ile	
				140					145					150	
Glu	Glu	Thr	Ile	Thr	Glu	Ser	Phe	Gly	Asn	Asp	His	Ser	Thr	Leu	
				155					160					165	
Asp	Gly	Tyr	Ser	Arg	Arg	Thr	Thr	Leu	Ser	Ser	Lys	Met	Tyr	His	
				170					175					180	
Thr	Lys	Gly	Gln	Glu	Gly	Ser	Val	Cys	Leu	Arg	Ser	Ser	Asp	Cys	
				185					190					195	
Ala	Ser	Gly	Leu	Cys	Cys	Ala	Arg	His	Phe	Trp	Ser	Lys	Ile	Cys	
				200					205					210	
Lys	Pro	Val	Leu	Lys	Glu	Gly	Gln	Val	Cys	Thr	Lys	His	Arg	Arg	
				215					220					225	
Lys	Gly	Ser	His	Gly	Leu	Glu	Ile	Phe	Gln	Arg	Cys	Tyr	Cys	Gly	
				230					235					240	
Glu	Gly	Leu	Ser	Cys	Arg	Ile	Gln	Lys	Asp	His	His	Gln	Ala	Ser	
				245					250					255	
Asn	Ser	Ser	Arg	Leu	His	Thr	Cys	Gln	Arg	His					
				260					265						

<210> 457  
 <211> 638  
 <212> DNA  
 <213> Homo sapiens  
  
 <220>  
 <221> unsure  
 <222> 30, 123, 133, 139, 180, 214, 259, 282, 308, 452, 467, 471, 473, 509, 556  
 <223> unknown base  
  
 <400> 457  
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 gcgcagcggg agctaaccgg gttttttgtn gcgatggtag cggcgggtttt 200



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<210> 459

<211> 747

<212> PRT

<213> Homo sapiens

<400> 459

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Arg	Ile	Ile	Leu	Cys	Phe	Leu	Ile	Val	Tyr	Met	Ala	Ile	Leu	Val	20	25	30	
Gly	Thr	Asp	Gln	Asp	Phe	Tyr	Ser	Leu	Leu	Gly	Val	Ser	Lys	Thr	35	40	45	
Ala	Ser	Ser	Arg	Glu	Ile	Arg	Gln	Ala	Phe	Lys	Lys	Leu	Ala	Leu	50	55	60	
Lys	Leu	His	Pro	Asp	Lys	Asn	Pro	Asn	Asn	Pro	Asn	Ala	His	Gly	65	70	75	
Asp	Phe	Leu	Lys	Ile	Asn	Arg	Ala	Tyr	Glu	Val	Leu	Lys	Asp	Glu	80	85	90	
Asp	Leu	Arg	Lys	Lys	Tyr	Asp	Lys	Tyr	Gly	Glu	Lys	Gly	Leu	Glu	95	100	105	
Asp	Asn	Gln	Gly	Gly	Gln	Tyr	Glu	Ser	Trp	Asn	Tyr	Tyr	Arg	Tyr	110	115	120	
Asp	Phe	Gly	Ile	Tyr	Asp	Asp	Asp	Pro	Glu	Ile	Ile	Thr	Leu	Glu	125	130	135	
Arg	Arg	Glu	Phe	Asp	Ala	Ala	Val	Asn	Ser	Gly	Glu	Leu	Trp	Phe	140	145	150	
Val	Asn	Phe	Tyr	Ser	Pro	Gly	Cys	Ser	His	Cys	His	Asp	Leu	Ala	155	160	165	
Pro	Thr	Trp	Arg	Asp	Phe	Ala	Lys	Glu	Val	Asp	Gly	Leu	Leu	Arg	170	175	180	
Ile	Gly	Ala	Val	Asn	Cys	Gly	Asp	Asp	Arg	Met	Leu	Cys	Arg	Met	185	190	195	
Lys	Gly	Val	Asn	Ser	Tyr	Pro	Ser	Leu	Phe	Ile	Phe	Arg	Ser	Gly				



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Met	Ala	Pro	Val	Lys 215	Tyr	His	Gly	Asp	Arg 220	Ser	Lys	Glu	Ser	Leu 225
Val	Ser	Phe	Ala	Met 230	Gln	His	Val	Arg	Ser 235	Thr	Val	Thr	Glu	Leu 240
Trp	Thr	Gly	Asn	Phe 245	Val	Asn	Ser	Ile	Gln 250	Thr	Ala	Phe	Ala	Ala 255
Gly	Ile	Gly	Trp	Leu 260	Ile	Thr	Phe	Cys	Ser 265	Lys	Gly	Gly	Asp	Cys 270
Leu	Thr	Ser	Gln	Thr 275	Arg	Leu	Arg	Leu	Ser 280	Gly	Met	Leu	Phe	Leu 285
Asn	Ser	Leu	Asp	Ala 290	Lys	Glu	Ile	Tyr	Leu 295	Glu	Val	Ile	His	Asn 300
Leu	Pro	Asp	Phe	Glu 305	Leu	Leu	Ser	Ala	Asn 310	Thr	Leu	Glu	Asp	Arg 315
Leu	Ala	His	His	Arg 320	Trp	Leu	Leu	Phe	Phe 325	His	Phe	Gly	Lys	Asn 330
Glu	Asn	Ser	Asn	Asp 335	Pro	Glu	Leu	Lys	Lys 340	Leu	Lys	Thr	Leu	Leu 345
Lys	Asn	Asp	His	Ile 350	Gln	Val	Gly	Arg	Phe 355	Asp	Cys	Ser	Ser	Ala 360
Pro	Asp	Ile	Cys	Ser 365	Asn	Leu	Tyr	Val	Phe 370	Gln	Pro	Ser	Leu	Ala 375
Val	Phe	Lys	Gly	Gln 380	Gly	Thr	Lys	Glu	Tyr 385	Glu	Ile	His	His	Gly 390
Lys	Lys	Ile	Leu	Tyr 395	Asp	Ile	Leu	Ala	Phe 400	Ala	Lys	Glu	Ser	Val 405
Asn	Ser	His	Val	Thr 410	Thr	Leu	Gly	Pro	Gln 415	Asn	Phe	Pro	Ala	Asn 420
Asp	Lys	Glu	Pro	Trp 425	Leu	Val	Asp	Phe	Phe 430	Ala	Pro	Trp	Cys	Pro 435
Pro	Cys	Arg	Ala	Leu 440	Leu	Pro	Glu	Leu	Arg 445	Arg	Ala	Ser	Asn	Leu 450
Leu	Tyr	Gly	Gln	Leu 455	Lys	Phe	Gly	Thr	Leu 460	Asp	Cys	Thr	Val	His 465
Glu	Gly	Leu	Cys	Asn 470	Met	Tyr	Asn	Ile	Gln 475	Ala	Tyr	Pro	Thr	Thr 480
Val	Val	Phe	Asn	Gln 485	Ser	Asn	Ile	His	Glu 490	Tyr	Glu	Gly	His	His 495

Ser	Ala	Glu	Gln	Ile	Leu	Glu	Phe	Ile	Glu	Asp	Leu	Met	Asn	Pro	
				500					505					510	
Ser	Val	Val	Ser	Leu	Thr	Pro	Thr	Thr	Phe	Asn	Glu	Leu	Val	Thr	
				515					520					525	
Gln	Arg	Lys	His	Asn	Glu	Val	Trp	Met	Val	Asp	Phe	Tyr	Ser	Pro	
				530					535					540	
Trp	Cys	His	Pro	Cys	Gln	Val	Leu	Met	Pro	Glu	Trp	Lys	Arg	Met	
				545					550					555	
Ala	Arg	Thr	Leu	Thr	Gly	Leu	Ile	Asn	Val	Gly	Ser	Ile	Asp	Cys	
				560					565					570	
Gln	Gln	Tyr	His	Ser	Phe	Cys	Ala	Gln	Glu	Asn	Val	Gln	Arg	Tyr	
				575					580					585	
Pro	Glu	Ile	Arg	Phe	Phe	Pro	Pro	Lys	Ser	Asn	Lys	Ala	Tyr	Gln	
				590					595					600	
Tyr	His	Ser	Tyr	Asn	Gly	Trp	Asn	Arg	Asp	Ala	Tyr	Ser	Leu	Arg	
				605					610					615	
Ile	Trp	Gly	Leu	Gly	Phe	Leu	Pro	Gln	Val	Ser	Thr	Asp	Leu	Thr	
				620					625					630	
Pro	Gln	Thr	Phe	Ser	Glu	Lys	Val	Leu	Gln	Gly	Lys	Asn	His	Trp	
				635					640					645	
Val	Ile	Asp	Phe	Tyr	Ala	Pro	Trp	Cys	Gly	Pro	Cys	Gln	Asn	Phe	
				650					655					660	
Ala	Pro	Glu	Phe	Glu	Leu	Leu	Ala	Arg	Met	Ile	Lys	Gly	Lys	Val	
				665					670					675	
Lys	Ala	Gly	Lys	Val	Asp	Cys	Gln	Ala	Tyr	Ala	Gln	Thr	Cys	Gln	
				680					685					690	
Lys	Ala	Gly	Ile	Arg	Ala	Tyr	Pro	Thr	Val	Lys	Phe	Tyr	Phe	Tyr	
				695					700					705	
Glu	Arg	Ala	Lys	Arg	Asn	Phe	Gln	Glu	Glu	Gln	Ile	Asn	Thr	Arg	
				710					715					720	
Asp	Ala	Lys	Ala	Ile	Ala	Ala	Leu	Ile	Ser	Glu	Lys	Leu	Glu	Thr	
				725					730					735	
Leu	Arg	Asn	Gln	Gly	Lys	Arg	Asn	Lys	Asp	Glu	Leu				
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<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

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actccccagg ctgttcacac tgcc 24

<210> 461  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 461  
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<210> 462  
<211> 50  
<212> DNA  
<213> Artificial Sequence

<220>  
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<210> 463  
<211> 1818  
<212> DNA  
<213> Homo sapiens

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caccatcatc tactcctact tggagtcggt ggtgaagttt ttcattcctc 150  
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Arg	Lys	Ser	Val	Ala	Gly	Glu	Ile	Val	Leu	Ile	Thr	Gly	Ala	Gly	
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His	Gly	Ile	Gly	Arg	Gln	Thr	Thr	Tyr	Glu	Phe	Ala	Lys	Arg	Gln	
				50					55					60	
Ser	Ile	Leu	Val	Leu	Trp	Asp	Ile	Asn	Lys	Arg	Gly	Val	Glu	Glu	
				65					70					75	
Thr	Ala	Ala	Glu	Cys	Arg	Lys	Leu	Gly	Val	Thr	Ala	His	Ala	Tyr	
				80					85					90	
Val	Val	Asp	Cys	Ser	Asn	Arg	Glu	Glu	Ile	Tyr	Arg	Ser	Leu	Asn	
				95					100					105	
Gln	Val	Lys	Lys	Glu	Val	Gly	Asp	Val	Thr	Ile	Val	Val	Asn	Asn	
				110					115					120	
Ala	Gly	Thr	Val	Tyr	Pro	Ala	Asp	Leu	Leu	Ser	Thr	Lys	Asp	Glu	
				125					130					135	
Glu	Ile	Thr	Lys	Thr	Phe	Glu	Val	Asn	Ile	Leu	Gly	His	Phe	Trp	
				140					145					150	
Ile	Thr	Lys	Ala	Leu	Leu	Pro	Ser	Met	Met	Glu	Arg	Asn	His	Gly	
				155					160					165	
His	Ile	Val	Thr	Val	Ala	Ser	Val	Cys	Gly	His	Glu	Gly	Ile	Pro	
				170					175					180	
Tyr	Leu	Ile	Pro	Tyr	Cys	Ser	Ser	Lys	Phe	Ala	Ala	Val	Gly	Phe	
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His	Arg	Gly	Leu	Thr	Ser	Glu	Leu	Gln	Ala	Leu	Gly	Lys	Thr	Gly	
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Ile	Lys	Thr	Ser	Cys	Leu	Cys	Pro	Val	Phe	Val	Asn	Thr	Gly	Phe	
				215					220					225	
Thr	Lys	Asn	Pro	Ser	Thr	Arg	Leu	Trp	Pro	Val	Leu	Glu	Thr	Asp	
				230					235					240	
Glu	Val	Val	Arg	Ser	Leu	Ile	Asp	Gly	Ile	Leu	Thr	Asn	Lys	Lys	
				245					250					255	
Met	Ile	Phe	Val	Pro	Ser	Tyr	Ile	Asn	Ile	Phe	Leu	Arg	Leu	Gln	
				260					265					270	
Lys	Phe	Leu	Pro	Glu	Arg	Ala	Ser	Ala	Ile	Leu	Asn	Arg	Met	Gln	
				275					280					285	
Asn	Ile	Gln	Phe	Glu	Ala	Val	Val	Gly	His	Lys	Ile	Lys	Met	Lys	
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<210> 465  
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 <212> DNA  
 <213> Homo sapiens

<400> 465

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<210> 466

<211> 414

<212> PRT

<213> Homo sapiens

<400> 466

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Ala Ala His Phe Tyr Leu His Thr Ser Phe Ser Arg Pro His Thr  
35 40 45

Gly Pro Pro Leu Pro Thr Pro Gly Pro Asp Arg Asp Arg Glu Leu  
50 55 60

Thr Ala Asp Ser Asp Val Asp Glu Phe Leu Asp Lys Phe Leu Ser  
65 70 75

Ala Gly Val Lys Gln Ser Asp Leu Pro Arg Lys Glu Thr Glu Gln  
80 85 90

Pro Pro Ala Pro Gly Ser Met Glu Glu Ser Val Arg Gly Tyr Asp  
95 100 105

Trp Ser Pro Arg Asp Ala Arg Arg Ser Pro Asp Gln Gly Arg Gln  
110 115 120

Gln Ala Glu Arg Arg Ser Val Leu Arg Gly Phe Cys Ala Asn Ser  
125 130 135

Ser Leu Ala Phe Pro Thr Lys Glu Arg Ala Phe Asp Asp Ile Pro  
140 145 150

Asn Ser Glu Leu Ser His Leu Ile Val Asp Asp Arg His Gly Ala  
155 160 165

Ile Tyr Cys Tyr Val Pro Lys Val Ala Cys Thr Asn Trp Lys Arg  
170 175 180

Val Met Ile Val Leu Ser Gly Ser Leu Leu His Arg Gly Ala Pro  
185 190 195

Tyr Arg Asp Pro Leu Arg Ile Pro Arg Glu His Val His Asn Ala  
200 205 210

Ser Ala His Leu Thr Phe Asn Lys Phe Trp Arg Arg Tyr Gly Lys  
215 220 225

Leu Ser Arg His Leu Met Lys Val Lys Leu Lys Lys Tyr Thr Lys  
230 235 240

Phe Leu Phe Val Arg Asp Pro Phe Val Arg Leu Ile Ser Ala Phe  
245 250 255

Arg Ser Lys Phe Glu Leu Glu Asn Glu Glu Phe Tyr Arg Lys Phe  
260 265 270

Ala Val Pro Met Leu Arg Leu Tyr Ala Asn His Thr Ser Leu Pro  
275 280 285

Ala Ser Ala Arg Glu Ala Phe Arg Ala Gly Leu Lys Val Ser Phe  
290 295 300

Ala Asn Phe Ile Gln Tyr Leu Leu Asp Pro His Thr Glu Lys Leu  
305 310 315

Ala Pro Phe Asn Glu His Trp Arg Gln Val Tyr Arg Leu Cys His  
320 325 330

Pro Cys Gln Ile Asp Tyr Asp Phe Val Gly Lys Leu Glu Thr Leu  
335 340 345

Asp Glu Asp Ala Ala Gln Leu Leu Gln Leu Leu Gln Val Asp Arg  
350 355 360

Gln Leu Arg Phe Pro Pro Ser Tyr Arg Asn Arg Thr Ala Ser Ser  
365 370 375

Trp Glu Glu Asp Trp Phe Ala Lys Ile Pro Leu Ala Trp Arg Gln  
380 385 390

Gln Leu Tyr Lys Leu Tyr Glu Ala Asp Phe Val Leu Phe Gly Tyr  
395 400 405

Pro Lys Pro Glu Asn Leu Leu Arg Asp  
410

<210> 467  
<211> 1071  
<212> DNA  
<213> Homo sapiens

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acgggatggc tacgggaacg cgctatgccg ggaaggtggt ggtcgtgacc 150  
gggggcgggc gcggcatcgg agctgggatc gtgcgcgcct tcgtgaacag 200  
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tggagcagga gctccctgga gctgtcttta tcctctgtga tgtgactcag 300  
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aaagcttttg ccctggatga aagtccatat ggtgtccgag tcaactgtat 650  
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tgccagaccc tagggccaca atccgagagg gcatgctggc ccagccactg 750  
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cagagctggg gtacgggtgc aaggccagtc ggagcacccc cgtggacgcc 900  
ccgatatacc ctctctgatt tctctcattt ctacttgggg ccccttcct 950  
aggactctcc cccccaaac tccaacctgt atcagatgca gcccccaagc 1000  
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ccataaaaac gatttgcagc c 1071

<210> 468

<211> 270

<212> PRT

<213> Homo sapiens

<400> 468

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Gly	Gly	Gly	Arg	Gly	Ile	Gly	Ala	Gly	Ile	Val	Arg	Ala	Phe	Val
				20					25					30
Asn	Ser	Gly	Ala	Arg	Val	Val	Ile	Cys	Asp	Lys	Asp	Glu	Ser	Gly
				35					40					45
Gly	Arg	Ala	Leu	Glu	Gln	Glu	Leu	Pro	Gly	Ala	Val	Phe	Ile	Leu
				50					55					60
Cys	Asp	Val	Thr	Gln	Glu	Asp	Asp	Val	Lys	Thr	Leu	Val	Ser	Glu
				65					70					75
Thr	Ile	Arg	Arg	Phe	Gly	Arg	Leu	Asp	Cys	Val	Val	Asn	Asn	Ala
				80					85					90
Gly	His	His	Pro	Pro	Pro	Gln	Arg	Pro	Glu	Glu	Thr	Ser	Ala	Gln
				95					100					105
Gly	Phe	Arg	Gln	Leu	Leu	Glu	Leu	Asn	Leu	Leu	Gly	Thr	Tyr	Thr
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Leu	Thr	Lys	Leu	Ala	Leu	Pro	Tyr	Leu	Arg	Lys	Ser	Gln	Gly	Asn	
				125					130					135	
Val	Ile	Asn	Ile	Ser	Ser	Leu	Val	Gly	Ala	Ile	Gly	Gln	Ala	Gln	
				140					145					150	
Ala	Val	Pro	Tyr	Val	Ala	Thr	Lys	Gly	Ala	Val	Thr	Ala	Met	Thr	
				155					160					165	
Lys	Ala	Leu	Ala	Leu	Asp	Glu	Ser	Pro	Tyr	Gly	Val	Arg	Val	Asn	
				170					175					180	
Cys	Ile	Ser	Pro	Gly	Asn	Ile	Trp	Thr	Pro	Leu	Trp	Glu	Glu	Leu	
				185					190					195	
Ala	Ala	Leu	Met	Pro	Asp	Pro	Arg	Ala	Thr	Ile	Arg	Glu	Gly	Met	
				200					205					210	
Leu	Ala	Gln	Pro	Leu	Gly	Arg	Met	Gly	Gln	Pro	Ala	Glu	Val	Gly	
				215					220					225	
Ala	Ala	Ala	Val	Phe	Leu	Ala	Ser	Glu	Ala	Asn	Phe	Cys	Thr	Gly	
				230					235					240	
Ile	Glu	Leu	Leu	Val	Thr	Gly	Gly	Ala	Glu	Leu	Gly	Tyr	Gly	Cys	
				245					250					255	
Lys	Ala	Ser	Arg	Ser	Thr	Pro	Val	Asp	Ala	Pro	Asp	Ile	Pro	Ser	
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 <211> 687  
 <212> DNA  
 <213> Homo sapiens

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 ccagcccagg agccccaaaa gcaagaggaa ggggcaaggg cggcctgggc 150  
 ccctggcccc tggccctcac caggtgccac tggacctggt gtcacggatg 200  
 aaaccgtatg cccgcatgga ggagtatgag aggaacatcg aggagatggt 250  
 ggcccagctg aggaacagct cagagctggc ccagagaaag tgtgaggtca 300  
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 agcatcaacc acgaccccag ccgtatcccc gtggacctgc cggaggcacg 400  
 gtgcctgtgt ctgggctgtg tgaaccctt caccatgcag gaggaccgca 450  
 gcatggtgag cgtgccggtg ttcagccagg ttcctgtgcg ccgccgctc 500  
 tgcccgccac cgccccgcac agggccttgc cgccagcgcg cagtcatgga 550



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 cgacggcagg ccccgaggag gccgcgctgc cgccggagca gagccgggtc 250  
 cagcccatga ccgcctccaa ctggacgctg gtgatggagg gcgagtggat 300  
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 aaggtagatg tcattcaaga accaggthtg agtggccgct tctttgtcac 450  
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Val	Asp	Val	Ile	Gln	Glu	Pro	Gly	Leu	Ser	Gly	Arg	Phe	Phe	Val
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Thr	Thr	Leu	Pro	Ala	Phe	Phe	His	Ala	Lys	Asp	Gly	Ile	Phe	Arg
				110					115					120
Arg	Tyr	Arg	Gly	Pro	Gly	Ile	Phe	Glu	Asp	Leu	Gln	Asn	Tyr	Ile
				125					130					135
Leu	Glu	Lys	Lys	Trp	Gln	Ser	Val	Glu	Pro	Leu	Thr	Gly	Trp	Lys
				140					145					150
Ser	Pro	Ala	Ser	Leu	Thr	Met	Ser	Gly	Met	Ala	Gly	Leu	Phe	Ser
				155					160					165
Ile	Ser	Gly	Lys	Ile	Trp	His	Leu	His	Asn	Tyr	Phe	Thr	Val	Thr
				170					175					180
Leu	Gly	Ile	Pro	Ala	Trp	Cys	Ser	Tyr	Val	Phe	Phe	Val	Ile	Ala
				185					190					195
Thr	Leu	Val	Phe	Gly	Leu	Phe	Met	Gly	Leu	Val	Leu	Val	Val	Ile
				200					205					210
Ser	Glu	Cys	Phe	Tyr	Val	Pro	Leu	Pro	Arg	His	Leu	Ser	Glu	Arg
				215					220					225
Ser	Glu	Gln	Asn	Arg	Arg	Ser	Glu	Glu	Ala	His	Arg	Ala	Glu	Gln
				230					235					240
Leu	Gln	Asp	Ala	Glu	Glu	Glu	Lys	Asp	Asp	Ser	Asn	Glu	Glu	Glu
				245					250					255
Asn	Lys	Asp	Ser	Leu	Val	Asp	Asp	Glu	Glu	Glu	Lys	Glu	Asp	Leu
				260					265					270
Gly	Asp	Glu	Asp	Glu	Ala	Glu	Glu	Glu	Glu	Glu	Glu	Asp	Asn	Leu
				275					280					285
Ala	Ala	Gly	Val	Asp	Glu	Glu	Arg	Ser	Glu	Ala	Asn	Asp	Gln	Gly
				290					295					300
Pro	Pro	Gly	Glu	Asp	Gly	Val	Thr	Arg	Glu	Glu	Val	Glu	Pro	Glu
				305					310					315
Glu	Ala	Glu	Glu	Gly	Ile	Ser	Glu	Gln	Pro	Cys	Pro	Ala	Asp	Thr
				320					325					330
Glu	Val	Val	Glu	Asp	Ser	Leu	Arg	Gln	Arg	Lys	Ser	Gln	His	Ala
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Asp	Lys	Gly	Leu											

<210> 473  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 473  
gtccagccca tgaccgcctc caac 24

<210> 474  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 474  
ctctctcat ccacaccagc agcc 24

<210> 475  
<211> 44  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 475  
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<210> 476  
<211> 2478  
<212> DNA  
<213> Homo sapiens

<400> 476  
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tcaagaacaa tggaatatca tcctgattta gaaaatttgg atgaagatgg 200  
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 cagccaagct tgagttttta ttttttattt atttattttt ttgagatagg 1050  
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<210> 477  
<211> 201  
<212> PRT  
<213> Homo sapiens

<400> 477

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Val	Ser	Glu	Lys	Gly	Ser	Cys	Ala	Ala	Ser	Pro	Pro	Trp	Arg	Leu	35	40	45	
Ile	Ala	Val	Ile	Leu	Gly	Ile	Leu	Cys	Leu	Val	Ile	Leu	Val	Ile	50	55	60	
Ala	Val	Val	Leu	Gly	Thr	Met	Gly	Val	Leu	Ser	Ser	Pro	Cys	Pro	65	70	75	
Pro	Asn	Trp	Ile	Ile	Tyr	Glu	Lys	Ser	Cys	Tyr	Leu	Phe	Ser	Met	80	85	90	
Ser	Leu	Asn	Ser	Trp	Asp	Gly	Ser	Lys	Arg	Gln	Cys	Trp	Gln	Leu	95	100	105	
Gly	Ser	Asn	Leu	Leu	Lys	Ile	Asp	Ser	Ser	Asn	Glu	Leu	Gly	Phe	110	115	120	
Ile	Val	Lys	Gln	Val	Ser	Ser	Gln	Pro	Asp	Asn	Ser	Phe	Trp	Ile	125	130	135	
Gly	Leu	Ser	Arg	Pro	Gln	Thr	Glu	Val	Pro	Trp	Leu	Trp	Glu	Asp	140	145	150	
Gly	Ser	Thr	Phe	Ser	Ser	Asn	Leu	Phe	Gln	Ile	Arg	Thr	Thr	Ala	155	160	165	
Thr	Gln	Glu	Asn	Pro	Ser	Pro	Asn	Cys	Val	Trp	Ile	His	Val	Ser				

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Val Ile Tyr Asp Gln Leu Cys Ser Val	Pro Ser Tyr Ser Ile Cys				
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Glu Lys Lys Phe Ser Met					
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<210> 478  
 <211> 27  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 478  
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<210> 479  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 479  
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<210> 480  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 480  
 atcctcccag agccatggta cctc 24

<210> 481  
 <211> 51  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 481  
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<210> 482  
 <211> 3819  
 <212> DNA  
 <213> Homo sapiens

341

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<210> 483  
 <211> 693  
 <212> PRT  
 <213> Homo sapiens

<400> 483  
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 20 25 30  
 Asp Phe Arg Phe Cys Ser Gln Arg Asn Gln Thr His Arg Ser Ser  
 35 40 45  
 Leu His Tyr Lys Pro Thr Pro Asp Leu Arg Ile Ser Ile Glu Asn  
 50 55 60  
 Ser Glu Glu Ala Leu Thr Val His Ala Pro Phe Pro Ala Ala His  
 65 70 75

Pro	Ala	Ser	Arg	Ser	Phe	Pro	Asp	Pro	Arg	Gly	Leu	Tyr	His	Phe	
				80					85					90	
Cys	Leu	Tyr	Trp	Asn	Arg	His	Ala	Gly	Arg	Leu	His	Leu	Leu	Tyr	
				95					100					105	
Gly	Lys	Arg	Asp	Phe	Leu	Leu	Ser	Asp	Lys	Ala	Ser	Ser	Leu	Leu	
				110					115					120	
Cys	Phe	Gln	His	Gln	Glu	Glu	Ser	Leu	Ala	Gln	Gly	Pro	Pro	Leu	
				125					130					135	
Leu	Ala	Thr	Ser	Val	Thr	Ser	Trp	Trp	Ser	Pro	Gln	Asn	Ile	Ser	
				140					145					150	
Leu	Pro	Ser	Ala	Ala	Ser	Phe	Thr	Phe	Ser	Phe	His	Ser	Pro	Pro	
				155					160					165	
His	Thr	Ala	Ala	His	Asn	Ala	Ser	Val	Asp	Met	Cys	Glu	Leu	Lys	
				170					175					180	
Arg	Asp	Leu	Gln	Leu	Leu	Ser	Gln	Phe	Leu	Lys	His	Pro	Gln	Lys	
				185					190					195	
Ala	Ser	Arg	Arg	Pro	Ser	Ala	Ala	Pro	Ala	Ser	Gln	Gln	Leu	Gln	
				200					205					210	
Ser	Leu	Glu	Ser	Lys	Leu	Thr	Ser	Val	Arg	Phe	Met	Gly	Asp	Met	
				215					220					225	
Val	Ser	Phe	Glu	Glu	Asp	Arg	Ile	Asn	Ala	Thr	Val	Trp	Lys	Leu	
				230					235					240	
Gln	Pro	Thr	Ala	Gly	Leu	Gln	Asp	Leu	His	Ile	His	Ser	Arg	Gln	
				245					250					255	
Glu	Glu	Glu	Gln	Ser	Glu	Ile	Met	Glu	Tyr	Ser	Val	Leu	Leu	Pro	
				260					265					270	
Arg	Thr	Leu	Phe	Gln	Arg	Thr	Lys	Gly	Arg	Ser	Gly	Glu	Ala	Glu	
				275					280					285	
Lys	Arg	Leu	Leu	Leu	Val	Asp	Phe	Ser	Ser	Gln	Ala	Leu	Phe	Gln	
				290					295					300	
Asp	Lys	Asn	Ser	Ser	Gln	Val	Leu	Gly	Glu	Lys	Val	Leu	Gly	Ile	
				305					310					315	
Val	Val	Gln	Asn	Thr	Lys	Val	Ala	Asn	Leu	Thr	Glu	Pro	Val	Val	
				320					325					330	
Leu	Thr	Phe	Gln	His	Gln	Leu	Gln	Pro	Lys	Asn	Val	Thr	Leu	Gln	
				335					340					345	
Cys	Val	Phe	Trp	Val	Glu	Asp	Pro	Thr	Leu	Ser	Ser	Pro	Gly	His	
				350					355					360	
Trp	Ser	Ser	Ala	Gly	Cys	Glu	Thr	Val	Arg	Arg	Glu	Thr	Gln	Thr	

				365					370					375
Ser	Cys	Phe	Cys	Asn 380	His	Leu	Thr	Tyr	Phe 385	Ala	Val	Leu	Met	Val 390
Ser	Ser	Val	Glu	Val 395	Asp	Ala	Val	His	Lys 400	His	Tyr	Leu	Ser	Leu 405
Leu	Ser	Tyr	Val	Gly 410	Cys	Val	Val	Ser	Ala 415	Leu	Ala	Cys	Leu	Val 420
Thr	Ile	Ala	Ala	Tyr 425	Leu	Cys	Ser	Arg	Val 430	Pro	Leu	Pro	Cys	Arg 435
Arg	Lys	Pro	Arg	Asp 440	Tyr	Thr	Ile	Lys	Val 445	His	Met	Asn	Leu	Leu 450
Leu	Ala	Val	Phe	Leu 455	Leu	Asp	Thr	Ser	Phe 460	Leu	Leu	Ser	Glu	Pro 465
Val	Ala	Leu	Thr	Gly 470	Ser	Glu	Ala	Gly	Cys 475	Arg	Ala	Ser	Ala	Ile 480
Phe	Leu	His	Phe	Ser 485	Leu	Leu	Thr	Cys	Leu 490	Ser	Trp	Met	Gly	Leu 495
Glu	Gly	Tyr	Asn	Leu 500	Tyr	Arg	Leu	Val	Val 505	Glu	Val	Phe	Gly	Thr 510
Tyr	Val	Pro	Gly	Tyr 515	Leu	Leu	Lys	Leu	Ser 520	Ala	Met	Gly	Trp	Gly 525
Phe	Pro	Ile	Phe	Leu 530	Val	Thr	Leu	Val	Ala 535	Leu	Val	Asp	Val	Asp 540
Asn	Tyr	Gly	Pro	Ile 545	Ile	Leu	Ala	Val	His 550	Arg	Thr	Pro	Glu	Gly 555
Val	Ile	Tyr	Pro	Ser 560	Met	Cys	Trp	Ile	Arg 565	Asp	Ser	Leu	Val	Ser 570
Tyr	Ile	Thr	Asn	Leu 575	Gly	Leu	Phe	Ser	Leu 580	Val	Phe	Leu	Phe	Asn 585
Met	Ala	Met	Leu	Ala 590	Thr	Met	Val	Val	Gln 595	Ile	Leu	Arg	Leu	Arg 600
Pro	His	Thr	Gln	Lys 605	Trp	Ser	His	Val	Leu 610	Thr	Leu	Leu	Gly	Leu 615
Ser	Leu	Val	Leu	Gly 620	Leu	Pro	Trp	Ala	Leu 625	Ile	Phe	Phe	Ser	Phe 630
Ala	Ser	Gly	Thr	Phe 635	Gln	Leu	Val	Val	Leu 640	Tyr	Leu	Phe	Ser	Ile 645
Ile	Thr	Ser	Phe	Gln 650	Gly	Phe	Leu	Ile	Phe 655	Ile	Trp	Tyr	Trp	Ser 660

345

Met Arg Leu Gln Ala Arg Gly Gly Pro Ser Pro Leu Lys Ser Asn  
665 670 675

Ser Asp Ser Ala Arg Leu Pro Ile Ser Ser Gly Ser Thr Ser Ser  
680 685 690

Ser Arg Ile

<210> 484  
<211> 516  
<212> DNA  
<213> Homo sapiens

<220>  
<221> unsure  
<222> 68, 70, 84, 147  
<223> unknown base

<400> 484  
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ctgccttgca gaggaaan cn tcgggactac acctcaagt gcacatgaac 100  
ctgctgctgg ccgtcttctt gctggacacg agcttcctgc tcagcgnagc 150  
cgggtggccct gacaggctct gaaggctggc tgccgagcca gtgccatctt 200  
cctgcacttc tctgctcac ctgcctttcc tggatgggcc tcgaggggta 250  
caacctctac cgactcgtgg tggaggctct tggcacctat gtccctggct 300  
acctactcaa gctgagcgcc atgggctggg gcttcccat ctttctggtg 350  
acgctggtgg ccctggtgga tgtggacaac tatggcccca tcatcttggc 400  
tgtgcatagg actccagagg gcgatcatcta cccttccatg tgctggatcc 450  
gggaactccct ggtcagctac atcaccaacc tgggcctctt cagcctggtg 500  
tttctgttca acatgg 516

<210> 485  
<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 485  
ggcattggag cagtgtggg tg 22

<210> 486  
<211> 24  
<212> DNA  
<213> Artificial Sequence



<220>  
<223> Synthetic oligonucleotide probe

<400> 486  
tggaggccta gatgcggctg gacg 24

<210> 487  
<211> 2849  
<212> DNA  
<213> Homo sapiens

<220>  
<221> unsure  
<222> 2715  
<223> unknown base

<400> 487  
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aagagggctc taggaaaaag ttttgatgg gattatgtgg aaactaccct 150  
gcgattctct gctgccagag caggctcggc gcttccaccc cagtgcagcc 200  
ttcccctggc ggtggtgaaa gagactcggg agtcgctgct tccaaagtgc 250  
ccgccgtgag tgagctctca cccagtcag ccaaagagc ctcttcgggc 300  
ttctcctgct gacatctgcc ctggccggcc agagacaggg gactcaggcg 350  
gaatccaacc tgagtagtaa attccagttt tccagcaaca aggaacagaa 400  
cggagtacaa gatcctcagc atgagagaat tattactgtg tctactaatg 450  
gaagtattca cagcccaagg tttcctcata cttatccaag aaatacggtc 500  
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gtttgatgaa agatttgggc ttgaagacc agaagatgac atatgcaagt 600  
atgattttgt agaagttgag gaaccagtg atggaactat attagggcgc 650  
tggtgtgggt ctggtactgt accaggaaaa cagatttcta aaggaaatca 700  
aattaggata agatttgtat ctgatgaata ttttccttct gaaccagggt 750  
tctgcatcca ctacaacatt gtcatgccac aattcacaga agctgtgagt 800  
ccttcagtgc tacccttctc agctttgcc ctggacctgc ttaataatgc 850  
tataactgcc tttagtacct tggaagacct tattcgatat cttgaaccag 900  
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cttggcaagg cttttgtttt tggaagaaaa tccagagtgg tggatctgaa 1000  
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cagtgtccat aaggggaagaa ctaaagagaa ccgataccat tttctggcca 1100  
 ggttgtctcc tggttaaacg ctgtggtggg aactgtgcct gttgtctcca 1150  
 caattgcaat gaatgtcaat gtgtcccaag caaagttact aaaaaatacc 1200  
 acgaggtcct tcagttgaga ccaaagaccg gtgtcagggg attgcacaaa 1250  
 tcactcaccg acgtggccct ggagcaccat gaggagtgtg actgtgtgtg 1300  
 cagagggagc acaggaggat agccgcacat ccaccagcag ctcttgccca 1350  
 gagctgtgca gtgcagtggc tgattctatt agagaacgta tgcgttatct 1400  
 ccatccttaa tctcagttgt ttgcttcaag gacctttcat cttcaggatt 1450  
 tacagtgcac tctgaaagag gagacatcaa acagaattag gagttgtgca 1500  
 acagctcttt tgagaggagg cctaaaggac aggagaaaag gtcttcaatc 1550  
 gtggaaagaa aattaaatgt tgtattaaat agatcaccag ctagtttcag 1600  
 agttaccatg tacgtattcc actagctggg ttctgtatct cagttctttc 1650  
 gatacggcct agggtaatgt cagtacagga aaaaaactgt gcaagtgagc 1700  
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 atgtaaacca gaacattcta tgtactacaa acctggtttt taaaaaggaa 1850  
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 acaagatga tataaaatat tgttgctctg acaaaaatac atgtatttca 2250  
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 aagtagacat tcagatccag ccattactaa cctattcctt ttttggggaa 2450  
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 aaaatgctta atatngtgcc taggttatgt ggtgactatt tgaatcaaaa 2750  
 atgtattgaa tcatcaaata aaagaatgtg gctatttttg ggagaaaatt 2800  
 aaaaaaaaaa aaaaaaaaaa aggttttaggg ataacagggt aatgcggcc 2849

<210> 488  
 <211> 345  
 <212> PRT  
 <213> Homo sapiens

<400> 488  
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 20 25 30  
 Gln Phe Ser Ser Asn Lys Glu Gln Asn Gly Val Gln Asp Pro Gln  
 35 40 45  
 His Glu Arg Ile Ile Thr Val Ser Thr Asn Gly Ser Ile His Ser  
 50 55 60  
 Pro Arg Phe Pro His Thr Tyr Pro Arg Asn Thr Val Leu Val Trp  
 65 70 75  
 Arg Leu Val Ala Val Glu Glu Asn Val Trp Ile Gln Leu Thr Phe  
 80 85 90  
 Asp Glu Arg Phe Gly Leu Glu Asp Pro Glu Asp Asp Ile Cys Lys  
 95 100 105  
 Tyr Asp Phe Val Glu Val Glu Glu Pro Ser Asp Gly Thr Ile Leu  
 110 115 120  
 Gly Arg Trp Cys Gly Ser Gly Thr Val Pro Gly Lys Gln Ile Ser  
 125 130 135  
 Lys Gly Asn Gln Ile Arg Ile Arg Phe Val Ser Asp Glu Tyr Phe  
 140 145 150  
 Pro Ser Glu Pro Gly Phe Cys Ile His Tyr Asn Ile Val Met Pro  
 155 160 165  
 Gln Phe Thr Glu Ala Val Ser Pro Ser Val Leu Pro Pro Ser Ala  
 170 175 180  
 Leu Pro Leu Asp Leu Leu Asn Asn Ala Ile Thr Ala Phe Ser Thr  
 185 190 195

Leu	Glu	Asp	Leu	Ile	Arg	Tyr	Leu	Glu	Pro	Glu	Arg	Trp	Gln	Leu	
				200					205					210	
Asp	Leu	Glu	Asp	Leu	Tyr	Arg	Pro	Thr	Trp	Gln	Leu	Leu	Gly	Lys	
				215					220					225	
Ala	Phe	Val	Phe	Gly	Arg	Lys	Ser	Arg	Val	Val	Asp	Leu	Asn	Leu	
				230					235					240	
Leu	Thr	Glu	Glu	Val	Arg	Leu	Tyr	Ser	Cys	Thr	Pro	Arg	Asn	Phe	
				245					250					255	
Ser	Val	Ser	Ile	Arg	Glu	Glu	Leu	Lys	Arg	Thr	Asp	Thr	Ile	Phe	
				260					265					270	
Trp	Pro	Gly	Cys	Leu	Leu	Val	Lys	Arg	Cys	Gly	Gly	Asn	Cys	Ala	
				275					280					285	
Cys	Cys	Leu	His	Asn	Cys	Asn	Glu	Cys	Gln	Cys	Val	Pro	Ser	Lys	
				290					295					300	
Val	Thr	Lys	Lys	Tyr	His	Glu	Val	Leu	Gln	Leu	Arg	Pro	Lys	Thr	
				305					310					315	
Gly	Val	Arg	Gly	Leu	His	Lys	Ser	Leu	Thr	Asp	Val	Ala	Leu	Glu	
				320					325					330	
His	His	Glu	Glu	Cys	Asp	Cys	Val	Cys	Arg	Gly	Ser	Thr	Gly	Gly	
				335					340					345	

<210> 489

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 489

acttctcagt gtccataagg g 21

<210> 490

<211> 40

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 490

gaactaaaga gaaccgatac cattttctgg ccaggttgtc 40

<210> 491

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 491

caccacagcg tttaaccagg 20

<210> 492

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 492

acaacaggca cagttccac 20

<210> 493

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 493

ggcggaatcc aacctgagta g 21

<210> 494

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 494

gcggctatcc tcctgtgctc 20

<210> 495

<211> 3283

<212> DNA

<213> Homo sapiens

<400> 495

cccatctcaa gctgatcttg gcacctctca tgctctgctc tcttcaacca 50

gacctctaca ttccattttg gaagaagact aaaaatgggtg tttccaatgt 100

ggacactgaa gagacaaatt cttatccttt ttaacataat cctaatttcc 150

aaactccttg gggctagatg gtttcctaaa actctgccct gtgatgtcac 200

tctggatgtt ccaaagaacc atgtgatcgt ggactgcaca gacaagcatt 250

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 ggtcaaaaaa caacatgtgc atcaagaggc tgcagattaa acccagaagc 450  
 tttagtggac tcaacttattt aaaatccott tacctggatg gaaaccagct 500  
 actagagata cgcaggggcc tccgcctag cttacagctt ctcagccttg 550  
 aggccaacaa catcttttcc atcagaaaag agaattctaac agaactggcc 600  
 aacatagaaa tactctacct gggccaaaac tggttattatc gaaatccttg 650  
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 ggcctatagt caggtgttca aggaaacggt ctagcccttc tttgcaaac 3250

<211> 1049

<213> Homo sapiens

Met Val Phe Pro Met Trp Thr Leu Lys Arg Gln Ile Leu Ile Leu  
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Pro Lys Thr Leu Pro Cys Asp Val Thr Leu Asp Val Pro Lys Asn  
35 40 45

His Val Ile Val Asp Cys Thr Asp Lys His Leu Thr Glu Ile Pro  
50 55 60

Gly Gly Ile Pro Thr Asn Thr Thr Asn Leu Thr Leu Thr Ile Asn  
65 70 75

His Ile Pro Asp Ile Ser Pro Ala Ser Phe His Arg Leu Asp His  
80 85 90

Leu Val Glu Ile Asp Phe Arg Cys Asn Cys Val Pro Ile Pro Leu  
95 100 105

Gly Ser Lys Asn Asn Met Cys Ile Lys Arg Leu Gln Ile Lys Pro  
110 115 120

Arg Ser Phe Ser Gly Leu Thr Tyr Leu Lys Ser Leu Tyr Leu Asp  
125 130 135

Gly Asn Gln Leu Leu Glu Ile Pro Gln Gly Leu Pro Pro Ser Leu  
140 145 150

Gln Leu Leu Ser Leu Glu Ala Asn Asn Ile Phe Ser Ile Arg Lys  
155 160 165

Glu Asn Leu Thr Glu Leu Ala Asn Ile Glu Ile Leu Tyr Leu Gly  
170 175 180

Gln Asn Cys Tyr Tyr Arg Asn Pro Cys Tyr Val Ser Tyr Ser Ile  
185 190 195

Glu Lys Asp Ala Phe Leu Asn Leu Thr Lys Leu Lys Val Leu Ser  
200 205 210

Leu Lys Asp Asn Asn Val Thr Ala Val Pro Thr Val Leu Pro Ser  
215 220 225

Thr Leu Thr Glu Leu Tyr Leu Tyr Asn Asn Met Ile Ala Lys Ile  
230 235 240

Gln Glu Asp Asp Phe Asn Asn Leu Asn Gln Leu Gln Ile Leu Asp  
245 250 255



Leu	Ser	Gly	Asn	Cys	Pro	Arg	Cys	Tyr	Asn	Ala	Pro	Phe	Pro	Cys	
				260					265					270	
Ala	Pro	Cys	Lys	Asn	Asn	Ser	Pro	Leu	Gln	Ile	Pro	Val	Asn	Ala	
				275					280					285	
Phe	Asp	Ala	Leu	Thr	Glu	Leu	Lys	Val	Leu	Arg	Leu	His	Ser	Asn	
				290					295					300	
Ser	Leu	Gln	His	Val	Pro	Pro	Arg	Trp	Phe	Lys	Asn	Ile	Asn	Lys	
				305					310					315	
Leu	Gln	Glu	Leu	Asp	Leu	Ser	Gln	Asn	Phe	Leu	Ala	Lys	Glu	Ile	
				320					325					330	
Gly	Asp	Ala	Lys	Phe	Leu	His	Phe	Leu	Pro	Ser	Leu	Ile	Gln	Leu	
				335					340					345	
Asp	Leu	Ser	Phe	Asn	Phe	Glu	Leu	Gln	Val	Tyr	Arg	Ala	Ser	Met	
				350					355					360	
Asn	Leu	Ser	Gln	Ala	Phe	Ser	Ser	Leu	Lys	Ser	Leu	Lys	Ile	Leu	
				365					370					375	
Arg	Ile	Arg	Gly	Tyr	Val	Phe	Lys	Glu	Leu	Lys	Ser	Phe	Asn	Leu	
				380					385					390	
Ser	Pro	Leu	His	Asn	Leu	Gln	Asn	Leu	Glu	Val	Leu	Asp	Leu	Gly	
				395					400					405	
Thr	Asn	Phe	Ile	Lys	Ile	Ala	Asn	Leu	Ser	Met	Phe	Lys	Gln	Phe	
				410					415					420	
Lys	Arg	Leu	Lys	Val	Ile	Asp	Leu	Ser	Val	Asn	Lys	Ile	Ser	Pro	
				425					430					435	
Ser	Gly	Asp	Ser	Ser	Glu	Val	Gly	Phe	Cys	Ser	Asn	Ala	Arg	Thr	
				440					445					450	
Ser	Val	Glu	Ser	Tyr	Glu	Pro	Gln	Val	Leu	Glu	Gln	Leu	His	Tyr	
				455					460					465	
Phe	Arg	Tyr	Asp	Lys	Tyr	Ala	Arg	Ser	Cys	Arg	Phe	Lys	Asn	Lys	
				470					475					480	
Glu	Ala	Ser	Phe	Met	Ser	Val	Asn	Glu	Ser	Cys	Tyr	Lys	Tyr	Gly	
				485					490					495	
Gln	Thr	Leu	Asp	Leu	Ser	Lys	Asn	Ser	Ile	Phe	Phe	Val	Lys	Ser	
				500					505					510	
Ser	Asp	Phe	Gln	His	Leu	Ser	Phe	Leu	Lys	Cys	Leu	Asn	Leu	Ser	
				515					520					525	
Gly	Asn	Leu	Ile	Ser	Gln	Thr	Leu	Asn	Gly	Ser	Glu	Phe	Gln	Pro	
				530					535					540	
Leu	Ala	Glu	Leu	Arg	Tyr	Leu	Asp	Phe	Ser	Asn	Asn	Arg	Leu	Asp	

545

550

555

Leu Leu His Ser Thr Ala Phe Glu Glu Leu His Lys Leu Glu Val  
560 565 570

Leu Asp Ile Ser Ser Asn Ser His Tyr Phe Gln Ser Glu Gly Ile  
575 580 585

Thr His Met Leu Asn Phe Thr Lys Asn Leu Lys Val Leu Gln Lys  
590 595 600

Leu Met Met Asn Asp Asn Asp Ile Ser Ser Ser Thr Ser Arg Thr  
605 610 615

Met Glu Ser Glu Ser Leu Arg Thr Leu Glu Phe Arg Gly Asn His  
620 625 630

Leu Asp Val Leu Trp Arg Glu Gly Asp Asn Arg Tyr Leu Gln Leu  
635 640 645

Phe Lys Asn Leu Leu Lys Leu Glu Glu Leu Asp Ile Ser Lys Asn  
650 655 660

Ser Leu Ser Phe Leu Pro Ser Gly Val Phe Asp Gly Met Pro Pro  
665 670 675

Asn Leu Lys Asn Leu Ser Leu Ala Lys Asn Gly Leu Lys Ser Phe  
680 685 690

Ser Trp Lys Lys Leu Gln Cys Leu Lys Asn Leu Glu Thr Leu Asp  
695 700 705

Leu Ser His Asn Gln Leu Thr Thr Val Pro Glu Arg Leu Ser Asn  
710 715 720

Cys Ser Arg Ser Leu Lys Asn Leu Ile Leu Lys Asn Asn Gln Ile  
725 730 735

Arg Ser Leu Thr Lys Tyr Phe Leu Gln Asp Ala Phe Gln Leu Arg  
740 745 750

Tyr Leu Asp Leu Ser Ser Asn Lys Ile Gln Met Ile Gln Lys Thr  
755 760 765

Ser Phe Pro Glu Asn Val Leu Asn Asn Leu Lys Met Leu Leu Leu  
770 775 780

His His Asn Arg Phe Leu Cys Thr Cys Asp Ala Val Trp Phe Val  
785 790 795

Trp Trp Val Asn His Thr Glu Val Thr Ile Pro Tyr Leu Ala Thr  
800 805 810

Asp Val Thr Cys Val Gly Pro Gly Ala His Lys Gly Gln Ser Val  
815 820 825

Ile Ser Leu Asp Leu Tyr Thr Cys Glu Leu Asp Leu Thr Asn Leu  
830 835 840

Ile	Leu	Phe	Ser	Leu	Ser	Ile	Ser	Val	Ser	Leu	Phe	Leu	Met	Val	
				845					850					855	
Met	Met	Thr	Ala	Ser	His	Leu	Tyr	Phe	Trp	Asp	Val	Trp	Tyr	Ile	
				860					865					870	
Tyr	His	Phe	Cys	Lys	Ala	Lys	Ile	Lys	Gly	Tyr	Gln	Arg	Leu	Ile	
				875					880					885	
Ser	Pro	Asp	Cys	Cys	Tyr	Asp	Ala	Phe	Ile	Val	Tyr	Asp	Thr	Lys	
				890					895					900	
Asp	Pro	Ala	Val	Thr	Glu	Trp	Val	Leu	Ala	Glu	Leu	Val	Ala	Lys	
				905					910					915	
Leu	Glu	Asp	Pro	Arg	Glu	Lys	His	Phe	Asn	Leu	Cys	Leu	Glu	Glu	
				920					925					930	
Arg	Asp	Trp	Leu	Pro	Gly	Gln	Pro	Val	Leu	Glu	Asn	Leu	Ser	Gln	
				935					940					945	
Ser	Ile	Gln	Leu	Ser	Lys	Lys	Thr	Val	Phe	Val	Met	Thr	Asp	Lys	
				950					955					960	
Tyr	Ala	Lys	Thr	Glu	Asn	Phe	Lys	Ile	Ala	Phe	Tyr	Leu	Ser	His	
				965					970					975	
Gln	Arg	Leu	Met	Asp	Glu	Lys	Val	Asp	Val	Ile	Ile	Leu	Ile	Phe	
				980					985					990	
Leu	Glu	Lys	Pro	Phe	Gln	Lys	Ser	Lys	Phe	Leu	Gln	Leu	Arg	Lys	
				995					1000					1005	
Arg	Leu	Cys	Gly	Ser	Ser	Val	Leu	Glu	Trp	Pro	Thr	Asn	Pro	Gln	
				1010					1015					1020	
Ala	His	Pro	Tyr	Phe	Trp	Gln	Cys	Leu	Lys	Asn	Ala	Leu	Ala	Thr	
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 <212> DNA  
 <213> Homo sapiens

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 cctgctaata tctggttcct gtgagttatg cgccgaagaa aatttttcta 150  
 gaagctatcc ttgtgatgag aaaaagcaaa atgactcagt tattgcagag 200  
 tgcagcaatc gtcgactaca ggaagttccc caaacggtgg gcaaatatgt 250



gctcttactg aattgtccga cttggaagtt ctagatctca gctataattc 1750  
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 atttcacaaa tctaaaagtt ttaaacttga gccacaacaa catttatact 1850  
 ttaacagata agtataacct ggaaagcaag tccctggtag aattagtttt 1900  
 cagtggcaat cgccttgaca ttttgtggaa tgatgatgac aacaggata 1950  
 tctccatttt caaaggtctc aagaatctga cacgtctgga tttatccctt 2000  
 aataggctga agcacatccc aaatgaagca ttccttaatt tgccagcgag 2050  
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 tattgctatg taacaaatta tcccaaaact tagtggttta aaacaacaca 3300  
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<211> 1041

<212> PRT

<213> Homo sapiens

<400> 498

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Leu	Leu	Ile	Ser	Gly	Ser	Cys	Glu	Leu	Cys	Ala	Glu	Glu	Asn	Phe
				20					25					30

Ser	Arg	Ser	Tyr	Pro	Cys	Asp	Glu	Lys	Lys	Gln	Asn	Asp	Ser	Val
				35					40					45

Ile	Ala	Glu	Cys	Ser	Asn	Arg	Arg	Leu	Gln	Glu	Val	Pro	Gln	Thr
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

				50						55					60
Val	Gly	Lys	Tyr	Val	Thr	Glu	Leu	Asp	Leu	Ser	Asp	Asn	Phe	Ile	
				65					70					75	
Thr	His	Ile	Thr	Asn	Glu	Ser	Phe	Gln	Gly	Leu	Gln	Asn	Leu	Thr	
				80					85					90	
Lys	Ile	Asn	Leu	Asn	His	Asn	Pro	Asn	Val	Gln	His	Gln	Asn	Gly	
				95					100					105	
Asn	Pro	Gly	Ile	Gln	Ser	Asn	Gly	Leu	Asn	Ile	Thr	Asp	Gly	Ala	
				110					115					120	
Phe	Leu	Asn	Leu	Lys	Asn	Leu	Arg	Glu	Leu	Leu	Leu	Glu	Asp	Asn	
				125					130					135	
Gln	Leu	Pro	Gln	Ile	Pro	Ser	Gly	Leu	Pro	Glu	Ser	Leu	Thr	Glu	
				140					145					150	
Leu	Ser	Leu	Ile	Gln	Asn	Asn	Ile	Tyr	Asn	Ile	Thr	Lys	Glu	Gly	
				155					160					165	
Ile	Ser	Arg	Leu	Ile	Asn	Leu	Lys	Asn	Leu	Tyr	Leu	Ala	Trp	Asn	
				170					175					180	
Cys	Tyr	Phe	Asn	Lys	Val	Cys	Glu	Lys	Thr	Asn	Ile	Glu	Asp	Gly	
				185					190					195	
Val	Phe	Glu	Thr	Leu	Thr	Asn	Leu	Glu	Leu	Leu	Ser	Leu	Ser	Phe	
				200					205					210	
Asn	Ser	Leu	Ser	His	Val	Pro	Pro	Lys	Leu	Pro	Ser	Ser	Leu	Arg	
				215					220					225	
Lys	Leu	Phe	Leu	Ser	Asn	Thr	Gln	Ile	Lys	Tyr	Ile	Ser	Glu	Glu	
				230					235					240	
Asp	Phe	Lys	Gly	Leu	Ile	Asn	Leu	Thr	Leu	Leu	Asp	Leu	Ser	Gly	
				245					250					255	
Asn	Cys	Pro	Arg	Cys	Phe	Asn	Ala	Pro	Phe	Pro	Cys	Val	Pro	Cys	
				260					265					270	
Asp	Gly	Gly	Ala	Ser	Ile	Asn	Ile	Asp	Arg	Phe	Ala	Phe	Gln	Asn	
				275					280					285	
Leu	Thr	Gln	Leu	Arg	Tyr	Leu	Asn	Leu	Ser	Ser	Thr	Ser	Leu	Arg	
				290					295					300	
Lys	Ile	Asn	Ala	Ala	Trp	Phe	Lys	Asn	Met	Pro	His	Leu	Lys	Val	
				305					310					315	
Leu	Asp	Leu	Glu	Phe	Asn	Tyr	Leu	Val	Gly	Glu	Ile	Val	Ser	Gly	
				320					325					330	
Ala	Phe	Leu	Thr	Met	Leu	Pro	Arg	Leu	Glu	Ile	Leu	Asp	Leu	Ser	
				335					340					345	

Phe	Asn	Tyr	Ile	Lys	Gly	Ser	Tyr	Pro	Gln	His	Ile	Asn	Ile	Ser	350	355	360
Arg	Asn	Phe	Ser	Lys	Leu	Leu	Ser	Leu	Arg	Ala	Leu	His	Leu	Arg	365	370	375
Gly	Tyr	Val	Phe	Gln	Glu	Leu	Arg	Glu	Asp	Asp	Phe	Gln	Pro	Leu	380	385	390
Met	Gln	Leu	Pro	Asn	Leu	Ser	Thr	Ile	Asn	Leu	Gly	Ile	Asn	Phe	395	400	405
Ile	Lys	Gln	Ile	Asp	Phe	Lys	Leu	Phe	Gln	Asn	Phe	Ser	Asn	Leu	410	415	420
Glu	Ile	Ile	Tyr	Leu	Ser	Glu	Asn	Arg	Ile	Ser	Pro	Leu	Val	Lys	425	430	435
Asp	Thr	Arg	Gln	Ser	Tyr	Ala	Asn	Ser	Ser	Ser	Phe	Gln	Arg	His	440	445	450
Ile	Arg	Lys	Arg	Arg	Ser	Thr	Asp	Phe	Glu	Phe	Asp	Pro	His	Ser	455	460	465
Asn	Phe	Tyr	His	Phe	Thr	Arg	Pro	Leu	Ile	Lys	Pro	Gln	Cys	Ala	470	475	480
Ala	Tyr	Gly	Lys	Ala	Leu	Asp	Leu	Ser	Leu	Asn	Ser	Ile	Phe	Phe	485	490	495
Ile	Gly	Pro	Asn	Gln	Phe	Glu	Asn	Leu	Pro	Asp	Ile	Ala	Cys	Leu	500	505	510
Asn	Leu	Ser	Ala	Asn	Ser	Asn	Ala	Gln	Val	Leu	Ser	Gly	Thr	Glu	515	520	525
Phe	Ser	Ala	Ile	Pro	His	Val	Lys	Tyr	Leu	Asp	Leu	Thr	Asn	Asn	530	535	540
Arg	Leu	Asp	Phe	Asp	Asn	Ala	Ser	Ala	Leu	Thr	Glu	Leu	Ser	Asp	545	550	555
Leu	Glu	Val	Leu	Asp	Leu	Ser	Tyr	Asn	Ser	His	Tyr	Phe	Arg	Ile	560	565	570
Ala	Gly	Val	Thr	His	His	Leu	Glu	Phe	Ile	Gln	Asn	Phe	Thr	Asn	575	580	585
Leu	Lys	Val	Leu	Asn	Leu	Ser	His	Asn	Asn	Ile	Tyr	Thr	Leu	Thr	590	595	600
Asp	Lys	Tyr	Asn	Leu	Glu	Ser	Lys	Ser	Leu	Val	Glu	Leu	Val	Phe	605	610	615
Ser	Gly	Asn	Arg	Leu	Asp	Ile	Leu	Trp	Asn	Asp	Asp	Asp	Asn	Arg	620	625	630
Tyr	Ile	Ser	Ile	Phe	Lys	Gly	Leu	Lys	Asn	Leu	Thr	Arg	Leu	Asp			



				635					640					645
Leu	Ser	Leu	Asn	Arg	Leu	Lys	His	Ile	Pro	Asn	Glu	Ala	Phe	Leu
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Asn	Leu	Pro	Ala	Ser	Leu	Thr	Glu	Leu	His	Ile	Asn	Asp	Asn	Met
				665					670					675
Leu	Lys	Phe	Phe	Asn	Trp	Thr	Leu	Leu	Gln	Gln	Phe	Pro	Arg	Leu
				680					685					690
Glu	Leu	Leu	Asp	Leu	Arg	Gly	Asn	Lys	Leu	Leu	Phe	Leu	Thr	Asp
				695					700					705
Ser	Leu	Ser	Asp	Phe	Thr	Ser	Ser	Leu	Arg	Thr	Leu	Leu	Leu	Ser
				710					715					720
His	Asn	Arg	Ile	Ser	His	Leu	Pro	Ser	Gly	Phe	Leu	Ser	Glu	Val
				725					730					735
Ser	Ser	Leu	Lys	His	Leu	Asp	Leu	Ser	Ser	Asn	Leu	Leu	Lys	Thr
				740					745					750
Ile	Asn	Lys	Ser	Ala	Leu	Glu	Thr	Lys	Thr	Thr	Thr	Lys	Leu	Ser
				755					760					765
Met	Leu	Glu	Leu	His	Gly	Asn	Pro	Phe	Glu	Cys	Thr	Cys	Asp	Ile
				770					775					780
Gly	Asp	Phe	Arg	Arg	Trp	Met	Asp	Glu	His	Leu	Asn	Val	Lys	Ile
				785					790					795
Pro	Arg	Leu	Val	Asp	Val	Ile	Cys	Ala	Ser	Pro	Gly	Asp	Gln	Arg
				800					805					810
Gly	Lys	Ser	Ile	Val	Ser	Leu	Glu	Leu	Thr	Thr	Cys	Val	Ser	Asp
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Val	Thr	Ala	Val	Ile	Leu	Phe	Phe	Phe	Thr	Phe	Phe	Ile	Thr	Thr
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Met	Val	Met	Leu	Ala	Ala	Leu	Ala	His	His	Leu	Phe	Tyr	Trp	Asp
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Val	Trp	Phe	Ile	Tyr	Asn	Val	Cys	Leu	Ala	Lys	Val	Lys	Gly	Tyr
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Arg	Ser	Leu	Ser	Thr	Ser	Gln	Thr	Phe	Tyr	Asp	Ala	Tyr	Ile	Ser
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Tyr	Asp	Thr	Lys	Asp	Ala	Ser	Val	Thr	Asp	Trp	Val	Ile	Asn	Glu
				890					895					900
Leu	Arg	Tyr	His	Leu	Glu	Glu	Ser	Arg	Asp	Lys	Asn	Val	Leu	Leu
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Cys	Leu	Glu	Glu	Arg	Asp	Trp	Asp	Pro	Gly	Leu	Ala	Ile	Ile	Asp
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Asn	Leu	Met	Gln	Ser	Ile	Asn	Gln	Ser	Lys	Lys	Thr	Val	Phe	Val	
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Leu	Thr	Lys	Lys	Tyr	Ala	Lys	Ser	Trp	Asn	Phe	Lys	Thr	Ala	Phe	
				950					955					960	
Tyr	Leu	Ala	Leu	Gln	Arg	Leu	Met	Asp	Glu	Asn	Met	Asp	Val	Ile	
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Ile	Phe	Ile	Leu	Leu	Glu	Pro	Val	Leu	Gln	His	Ser	Gln	Tyr	Leu	
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Arg	Leu	Arg	Gln	Arg	Ile	Cys	Lys	Ser	Ser	Ile	Leu	Gln	Trp	Pro	
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Val	Val	Leu	Thr	Glu	Asn	Asp	Ser	Arg	Tyr	Asn	Asn	Met	Tyr	Val	
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<210> 504  
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gtgcctccag ggggccagtg ggcctgaggc cccagcaagg gctaggggtcc 200  
atctccagtc ccaggacaca gcagcggcca ccatggccac gcctgggctc 250  
cagcagcatc agcagcccc aggaccggg aggcacaggt ggccccacc 300  
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gcggcacaga gcagcctac cggcccggcc gtaggggtgtg tgctgtccg 500

gctcaogggg accctgtctc cgagtcgttc gtgcagcgtg tgtaccagcc 550  
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<210> 506  
<211> 273  
<212> PRT  
<213> Homo sapiens

<400> 506  
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Cys	Ala	Val	Arg	Ala	His	Gly	Asp	Pro	Val	Ser	Glu	Ser	Phe	Val	35	40	45
Gln	Arg	Val	Tyr	Gln	Pro	Phe	Leu	Thr	Thr	Cys	Asp	Gly	His	Arg	50	55	60
Ala	Cys	Ser	Thr	Tyr	Arg	Thr	Ile	Tyr	Arg	Thr	Ala	Tyr	Arg	Arg	65	70	75
Ser	Pro	Gly	Leu	Ala	Pro	Ala	Arg	Pro	Arg	Tyr	Ala	Cys	Cys	Pro	80	85	90
Gly	Trp	Lys	Arg	Thr	Ser	Gly	Leu	Pro	Gly	Ala	Cys	Gly	Ala	Ala	95	100	105
Ile	Cys	Gln	Pro	Pro	Cys	Arg	Asn	Gly	Gly	Ser	Cys	Val	Gln	Pro	110	115	120
Gly	Arg	Cys	Arg	Cys	Pro	Ala	Gly	Trp	Arg	Gly	Asp	Thr	Cys	Gln	125	130	135
Ser	Asp	Val	Asp	Glu	Cys	Ser	Ala	Arg	Arg	Gly	Gly	Cys	Pro	Gln	140	145	150
Arg	Cys	Ile	Asn	Thr	Ala	Gly	Ser	Tyr	Trp	Cys	Gln	Cys	Trp	Glu	155	160	165
Gly	His	Ser	Leu	Ser	Ala	Asp	Gly	Thr	Leu	Cys	Val	Pro	Lys	Gly	170	175	180
Gly	Pro	Pro	Arg	Val	Ala	Pro	Asn	Pro	Thr	Gly	Val	Asp	Ser	Ala	185	190	195
Met	Lys	Glu	Glu	Val	Gln	Arg	Leu	Gln	Ser	Arg	Val	Asp	Leu	Leu	200	205	210
Glu	Glu	Lys	Leu	Gln	Leu	Val	Leu	Ala	Pro	Leu	His	Ser	Leu	Ala	215	220	225
Ser	Gln	Ala	Leu	Glu	His	Gly	Leu	Pro	Asp	Pro	Gly	Ser	Leu	Leu	230	235	240
Val	His	Ser	Phe	Gln	Gln	Leu	Gly	Arg	Ile	Asp	Ser	Leu	Ser	Glu	245	250	255
Gln	Ile	Ser	Phe	Leu	Glu	Glu	Gln	Leu	Gly	Ser	Cys	Ser	Cys	Lys	260	265	270
Lys	Asp	Ser															

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 <211> 1700  
 <212> DNA  
 <213> Homo sapiens

<400> 507

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Glu	Glu	Lys	Leu	Gln	Leu	Val	Leu	Ala	Pro	Leu	His	Ser	Leu	Ala
				215					220					225
Ser	Gln	Ala	Leu	Glu	His	Gly	Leu	Pro	Asp	Pro	Gly	Ser	Leu	Leu
				230					235					240
Val	His	Ser	Phe	Gln	Gln	Leu	Gly	Arg	Ile	Asp	Ser	Leu	Ser	Glu
				245					250					255
Gln	Ile	Ser	Phe	Leu	Glu	Glu	Gln	Leu	Gly	Ser	Cys	Ser	Cys	Lys
				260					265					270

Lys Asp Ser

<210> 509  
 <211> 1538  
 <212> DNA  
 <213> Homo sapiens

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 ctgaggcccc agcaagggct aggggtccatc tccagtccca ggacacagca 150  
 gcggccacca tggccacgcc tgggctccag cagcatcagc agccccagg 200  
 accggggagg cacaggtggc ccccaccacc cggaggagca gctcctgccc 250  
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 ctgctgcctg acccccagca caataaaaat gaaacgtg 1538

<210> 510

<211> 273

<212> PRT

<213> Homo sapiens

<400> 510

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Ala	Val	Gly	Gly	Thr	Glu	His	Ala	Tyr	Arg	Pro	Gly	Arg	Arg	Val
				20					25					30
Cys	Ala	Val	Arg	Ala	His	Gly	Asp	Pro	Val	Ser	Glu	Ser	Phe	Val
				35					40					45
Gln	Arg	Val	Tyr	Gln	Pro	Phe	Leu	Thr	Thr	Cys	Asp	Gly	His	Arg
				50					55					60
Ala	Cys	Ser	Thr	Tyr	Arg	Thr	Ile	Tyr	Arg	Thr	Ala	Tyr	Arg	Arg
				65					70					75
Ser	Pro	Gly	Leu	Ala	Pro	Ala	Arg	Pro	Arg	Tyr	Ala	Cys	Cys	Pro
				80					85					90
Gly	Trp	Lys	Arg	Thr	Ser	Gly	Leu	Pro	Gly	Ala	Cys	Gly	Ala	Ala
				95					100					105
Ile	Cys	Gln	Pro	Pro	Cys	Arg	Asn	Gly	Gly	Ser	Cys	Val	Gln	Pro
				110					115					120
Gly	Arg	Cys	Arg	Cys	Pro	Ala	Gly	Trp	Arg	Gly	Asp	Thr	Cys	Gln
				125					130					135
Ser	Asp	Val	Asp	Glu	Cys	Ser	Ala	Arg	Arg	Gly	Gly	Cys	Pro	Gln







attatatgtg gctatatattc ctagagcacc tgtgttttcc tctttctaag 2600  
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<210> 515

<211> 364

<212> PRT

<213> Homo sapiens

<400> 515

Met	Ser	Val	Met	Val	Val	Arg	Lys	Lys	Val	Thr	Arg	Lys	Trp	Glu	1	5	10	15
Lys	Leu	Pro	Gly	Arg	Asn	Thr	Phe	Cys	Cys	Asp	Gly	Arg	Val	Met	20	25	30	
Met	Ala	Arg	Gln	Lys	Gly	Ile	Phe	Tyr	Leu	Thr	Leu	Phe	Leu	Ile	35	40	45	
Leu	Gly	Thr	Cys	Thr	Leu	Phe	Phe	Ala	Phe	Glu	Cys	Arg	Tyr	Leu	50	55	60	
Ala	Val	Gln	Leu	Ser	Pro	Ala	Ile	Pro	Val	Phe	Ala	Ala	Met	Leu	65	70	75	
Phe	Leu	Phe	Ser	Met	Ala	Thr	Leu	Leu	Arg	Thr	Ser	Phe	Ser	Asp	80	85	90	
Pro	Gly	Val	Ile	Pro	Arg	Ala	Leu	Pro	Asp	Glu	Ala	Ala	Phe	Ile	95	100	105	
Glu	Met	Glu	Ile	Glu	Ala	Thr	Asn	Gly	Ala	Val	Pro	Gln	Gly	Gln	110	115	120	
Arg	Pro	Pro	Pro	Arg	Ile	Lys	Asn	Phe	Gln	Ile	Asn	Asn	Gln	Ile	125	130	135	
Val	Lys	Leu	Lys	Tyr	Cys	Tyr	Thr	Cys	Lys	Ile	Phe	Arg	Pro	Pro	140	145	150	
Arg	Ala	Ser	His	Cys	Ser	Ile	Cys	Asp	Asn	Cys	Val	Glu	Arg	Phe	155	160	165	
Asp	His	His	Cys	Pro	Trp	Val	Gly	Asn	Cys	Val	Gly	Lys	Arg	Asn	170	175	180	
Tyr	Arg	Tyr	Phe	Tyr	Leu	Phe	Ile	Leu	Ser	Leu	Ser	Leu	Leu	Thr	185	190	195	
Ile	Tyr	Val	Phe	Ala	Phe	Asn	Ile	Val	Tyr	Val	Ala	Leu	Lys	Ser	200	205	210	
Leu	Lys	Ile	Gly	Phe	Leu	Glu	Thr	Leu	Lys	Glu	Thr	Pro	Gly	Thr	215	220	225	
Val	Leu	Glu	Val	Leu	Ile	Cys	Phe	Phe	Thr	Leu	Trp	Ser	Val	Val				

	230		235		240
Gly Leu Thr Gly	Phe His Thr Phe Leu	Val Ala Leu Asn Gln Thr			
	245	250			255
Thr Asn Glu Asp	Ile Lys Gly Ser Trp	Thr Gly Lys Asn Arg Val			
	260	265			270
Gln Asn Pro Tyr	Ser His Gly Asn Ile	Val Lys Asn Cys Cys Glu			
	275	280			285
Val Leu Cys Gly	Pro Leu Pro Pro Ser	Val Leu Asp Arg Arg Gly			
	290	295			300
Ile Leu Pro Leu	Glu Glu Ser Gly Ser	Arg Pro Pro Ser Thr Gln			
	305	310			315
Glu Thr Ser Ser	Ser Leu Leu Pro Gln	Ser Pro Ala Pro Thr Glu			
	320	325			330
His Leu Asn Ser	Asn Glu Met Pro Glu	Asp Ser Ser Thr Pro Glu			
	335	340			345
Glu Met Pro Pro	Pro Glu Pro Pro Glu	Pro Pro Gln Glu Ala Ala			
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Glu Ala Glu Lys					

<210> 516  
 <211> 255  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> unsure  
 <222> 36, 38, 88, 118, 135, 193, 213, 222  
 <223> unknown base

<400> 516  
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 cccctgggtg gggaattgtg ttggaaagag gaactaccgc tanttctacc 200  
 tcttcacact ttntctctcc cncctcaca tctatgtctt cgccttcaac 250  
 atcgt 255

<210> 517  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>

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<223> Synthetic oligonucleotide probe

<400> 517
caacgtgatt tcaaagctgg gctc 24

<210> 518
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 518
gcctcgtatc aagaatttcc 20

<210> 519
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 519
agtggaaagtc gacctccc 18

<210> 520
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 520
ctcacctgaa atctctcata gccc 24

<210> 521
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 521
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<210> 522
<211> 1679
<212> DNA
<213> Homo sapiens

<400> 522
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agagcaacac aatctatcag gaaagaaaga aagaaaaaaa ccgaacctga 100

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<210> 523  
 <211> 344  
 <212> PRT  
 <213> Homo sapiens

<400> 523  
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 Val Arg Ser Gly Asp Ala Thr Phe Pro Lys Ala Met Asp Asn Val  
 35 40 45  
 Thr Val Arg Gln Gly Glu Ser Ala Thr Leu Arg Cys Thr Ile Asp  
 50 55 60  
 Asn Arg Val Thr Arg Val Ala Trp Leu Asn Arg Ser Thr Ile Leu  
 65 70 75  
 Tyr Ala Gly Asn Asp Lys Trp Cys Leu Asp Pro Arg Val Val Leu  
 80 85 90  
 Leu Ser Asn Thr Gln Thr Gln Tyr Ser Ile Glu Ile Gln Asn Val  
 95 100 105  
 Asp Val Tyr Asp Glu Gly Pro Tyr Thr Cys Ser Val Gln Thr Asp  
 110 115 120  
 Asn His Pro Lys Thr Ser Arg Val His Leu Ile Val Gln Val Ser  
 125 130 135  
 Pro Lys Ile Val Glu Ile Ser Ser Asp Ile Ser Ile Asn Glu Gly  
 140 145 150  
 Asn Asn Ile Ser Leu Thr Cys Ile Ala Thr Gly Arg Pro Glu Pro  
 155 160 165  
 Thr Val Thr Trp Arg His Ile Ser Pro Lys Ala Val Gly Phe Val  
 170 175 180  
 Ser Glu Asp Glu Tyr Leu Glu Ile Gln Gly Ile Thr Arg Glu Gln  
 185 190 195  
 Ser Gly Asp Tyr Glu Cys Ser Ala Ser Asn Asp Val Ala Ala Pro  
 200 205 210  
 Val Val Arg Arg Val Lys Val Thr Val Asn Tyr Pro Pro Tyr Ile  
 215 220 225  
 Ser Glu Ala Lys Gly Thr Gly Val Pro Val Gly Gln Lys Gly Thr

230	235	240
Leu Gln Cys Glu Ala Ser Ala Val Pro	Ser Ala Glu Phe Gln Trp	
245	250	255
Tyr Lys Asp Asp Lys Arg Leu Ile Glu	Gly Lys Lys Gly Val Lys	
260	265	270
Val Glu Asn Arg Pro Phe Leu Ser Lys	Leu Ile Phe Phe Asn Val	
275	280	285
Ser Glu His Asp Tyr Gly Asn Tyr Thr	Cys Val Ala Ser Asn Lys	
290	295	300
Leu Gly His Thr Asn Ala Ser Ile Met	Leu Phe Gly Pro Gly Ala	
305	310	315
Val Ser Glu Val Ser Asn Gly Thr Ser	Arg Arg Ala Gly Cys Val	
320	325	330
Trp Leu Leu Pro Leu Leu Val Leu His	Leu Leu Leu Lys Phe	
335	340	

<210> 524  
 <211> 503  
 <212> DNA  
 <213> Homo sapiens

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<210> 525  
 <211> 2602  
 <212> DNA  
 <213> Homo sapiens

<400> 525  
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<400> 610  
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<210> 611  
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 <211> 352  
 <212> PRT  
 <213> Homo Sapien

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 Pro Ala Gly Gln Ser Val Asp Phe Pro Trp Ala Ala Val Asp Asn  
 35 40 45  
 Met Met Val Arg Lys Gly Asp Thr Ala Val Leu Arg Cys Tyr Leu  
 50 55 60  
 Glu Asp Gly Ala Ser Lys Gly Ala Trp Leu Asn Arg Ser Ser Ile  
 65 70 75  
 Ile Phe Ala Gly Gly Asp Lys Trp Ser Val Asp Pro Arg Val Ser  
 80 85 90  
 Ile Ser Thr Leu Asn Lys Arg Asp Tyr Ser Leu Gln Ile Gln Asn  
 95 100 105  
 Val Asp Val Thr Asp Asp Gly Pro Tyr Thr Cys Ser Val Gln Thr  
 110 115 120  
 Gln His Thr Pro Arg Thr Met Gln Val His Leu Thr Val Gln Val  
 125 130 135  
 Pro Pro Lys Ile Tyr Asp Ile Ser Asn Asp Met Thr Val Asn Glu  
 140 145 150  
 Gly Thr Asn Val Thr Leu Thr Cys Leu Ala Thr Gly Lys Pro Glu  
 155 160 165  
 Pro Ser Ile Ser Trp Arg His Ile Ser Pro Ser Ala Lys Pro Phe  
 170 175 180  
 Glu Asn Gly Gln Tyr Leu Asp Ile Tyr Gly Ile Thr Arg Asp Gln  
 185 190 195  
 Ala Gly Glu Tyr Glu Cys Ser Ala Glu Asn Ala Val Ser Phe Pro  
 200 205 210  
 Asp Val Arg Lys Val Lys Val Val Val Asn Phe Ala Pro Thr Ile  
 215 220 225  
 Gln Glu Ile Lys Ser Gly Thr Val Thr Pro Gly Arg Ser Gly Leu

1007067100401

230	235	240
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245	250	255
Tyr Lys Gly Glu Lys Lys Leu Phe Asn	Gly Gln Gln Gly Ile Ile	
260	265	270
Ile Gln Asn Phe Ser Thr Arg Ser Ile	Leu Thr Val Thr Asn Val	
275	280	285
Thr Gln Glu His Phe Gly Asn Tyr Thr	Cys Val Ala Ala Asn Lys	
290	295	300
Leu Gly Thr Thr Asn Ala Ser Leu Pro	Leu Asn Pro Pro Ser Thr	
305	310	315
Ala Gln Tyr Gly Ile Thr Gly Ser Ala	Asp Val Leu Phe Ser Cys	
320	325	330
Trp Tyr Leu Val Leu Thr Leu Ser Ser	Phe Thr Ser Ile Phe Tyr	
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 ctgcttttca ccaaattgca atggagcctt tcgaaatcaa tgttccaaag 200  
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 cccaggtctt caaggtcaca agggggccat gggcatgcct ggtgccctg 600  
 gcccgcggg accacctgct gagaaggag ccaagggggc tatgggacga 650

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ctggcacccc aggaccccaa ggagagaagg gcagcaaagg cgatgggggt 800  
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acctggactg caggggtgtc cgggccctcc tggtgcaagt ggacaccag 1050  
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<210> 614

<211> 520

<212> PRT

<213> Homo Sapien

<400> 614

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			20					25						30



Ile	Asn	Val	Pro	Lys	Pro	Lys	Arg	Arg	Asn	Gly	Val	Asn	Phe	Ser	35	40	45
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Gly	Leu	Leu	Val	Val	Gln	Val	Leu	Asn	Leu	Gln	Ala	Arg	Leu	Arg	65	70	75
Val	Leu	Glu	Met	Tyr	Phe	Leu	Asn	Asp	Thr	Leu	Ala	Ala	Glu	Asp	80	85	90
Ser	Pro	Ser	Phe	Ser	Leu	Leu	Gln	Ser	Ala	His	Pro	Gly	Glu	His	95	100	105
Leu	Ala	Gln	Gly	Ala	Ser	Arg	Leu	Gln	Val	Leu	Gln	Ala	Gln	Leu	110	115	120
Thr	Trp	Val	Arg	Val	Ser	His	Glu	His	Leu	Leu	Gln	Arg	Val	Asp	125	130	135
Asn	Phe	Thr	Gln	Asn	Pro	Gly	Met	Phe	Arg	Ile	Lys	Gly	Glu	Gln	140	145	150
Gly	Ala	Pro	Gly	Leu	Gln	Gly	His	Lys	Gly	Ala	Met	Gly	Met	Pro	155	160	165
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Gly	Ala	Met	Gly	Arg	Asp	Gly	Ala	Thr	Gly	Pro	Ser	Gly	Pro	Gln	185	190	195
Gly	Pro	Pro	Gly	Val	Lys	Gly	Glu	Ala	Gly	Leu	Gln	Gly	Pro	Gln	200	205	210
Gly	Ala	Pro	Gly	Lys	Gln	Gly	Ala	Thr	Gly	Thr	Pro	Gly	Pro	Gln	215	220	225
Gly	Glu	Lys	Gly	Ser	Lys	Gly	Asp	Gly	Gly	Leu	Ile	Gly	Pro	Lys	230	235	240
Gly	Glu	Thr	Gly	Thr	Lys	Gly	Glu	Lys	Gly	Asp	Leu	Gly	Leu	Pro	245	250	255
Gly	Ser	Lys	Gly	Asp	Arg	Gly	Met	Lys	Gly	Asp	Ala	Gly	Val	Met	260	265	270
Gly	Pro	Pro	Gly	Ala	Gln	Gly	Ser	Lys	Gly	Asp	Phe	Gly	Arg	Pro	275	280	285
Gly	Pro	Pro	Gly	Leu	Ala	Gly	Phe	Pro	Gly	Ala	Lys	Gly	Asp	Gln	290	295	300
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Gly Arg Lys Gly	Glu Ser Gly Val Pro	Gly Pro Ala Gly Val Lys			
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Gly Glu Gln Gly	Ser Pro Gly Leu Ala	Gly Pro Lys Gly Ala Pro			
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Gly Gln Ala Gly	Gln Lys Gly Asp Gln	Gly Val Lys Gly Ser Ser			
	395		400		405
Gly Glu Gln Gly	Val Lys Gly Glu Lys	Gly Glu Arg Gly Glu Asn			
	410		415		420
Ser Val Ser Val	Arg Ile Val Gly Ser	Ser Asn Arg Gly Arg Ala			
	425		430		435
Glu Val Tyr Tyr	Ser Gly Thr Trp Gly	Thr Ile Cys Asp Asp Glu			
	440		445		450
Trp Gln Asn Ser	Asp Ala Ile Val Phe	Cys Arg Met Leu Gly Tyr			
	455		460		465
Ser Lys Gly Arg	Ala Leu Tyr Lys Val	Gly Ala Gly Thr Gly Gln			
	470		475		480
Ile Trp Leu Asp	Asn Val Gln Cys Arg	Gly Thr Glu Ser Thr Leu			
	485		490		495
Trp Ser Cys Thr	Lys Asn Ser Trp Gly	His His Asp Cys Ser His			
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Glu Glu Asp Ala	Gly Val Glu Cys Ser Val				
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 <213> Homo Sapien

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 aaaagccaaa atgaaactga tggacttgt tttcaccatt gggctaactt 200  
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<210> 616  
 <211> 98  
 <212> PRT  
 <213> Homo Sapien

<400> 616  
 Met Lys Leu Met Val Leu Val Phe Thr Ile Gly Leu Thr Leu Leu  
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 Leu Gly Val Gln Ala Met Pro Ala Asn Arg Leu Ser Cys Tyr Arg  
 20 25 30  
 Lys Ile Leu Lys Asp His Asn Cys His Asn Leu Pro Glu Gly Val  
 35 40 45  
 Ala Asp Leu Thr Gln Ile Asp Val Asn Val Gln Asp His Phe Trp  
 50 55 60  
 Asp Gly Lys Gly Cys Glu Met Ile Cys Tyr Cys Asn Phe Ser Glu  
 65 70 75  
 Leu Leu Cys Cys Pro Lys Asp Val Phe Phe Gly Pro Lys Ile Ser  
 80 85 90  
 Phe Val Ile Pro Cys Asn Asn Gln  
 95

<210> 617  
 <211> 2558  
 <212> DNA  
 <213> Homo Sapien

<400> 617  
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 accccgccgt ggtggttga gggcgcgag tagagcagca gcacaggcgc 150  
 ggggtcccggg aggccggctc tgctcgcgcc gagatgtgga atctccttca 200  
 cgaaaccgac tcggctgtgg ccaccgcgcg ccgcccgcgc tggctgtgcg 250  
 ctggggcgct ggtgctggcg ggtggcttct ttctcctcgg cttcctcttc 300

gggtggttta taaaatcctc caatgaagct actaacatta ctccaaagca 350  
 taatatgaaa gcatttttgg atgaattgaa agctgagaac atcaagaagt 400  
 tcttacataa ttttacacag ataccacatt tagcaggaac agaacaaaac 450  
 tttcagcttg caaagcaaatt tcaatcccag tggaaagaat ttggcctgga 500  
 ttctgttgag ctagctcatt atgatgtcct gttgtcctac ccaaataaga 550  
 ctcatcccaa ctacatctca ataattaatg aagatggaaa tgagattttc 600  
 aacacatcat tatttgaacc acctcctcca ggatatgaaa atgtttcgga 650  
 tattgtacca cctttcagtg ctttctctcc tcaaggaatg ccagagggcg 700  
 atctagtgtg tgttaactat gcaogaaactg aagacttctt taaattggaa 750  
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 cagcaaattg atatgcttat aggcgtggaa ttgcagaggc tgttggtctt 1050  
 ccaagtattc ctgttcatcc aattggatac tatgatgcac agaagctcct 1100  
 agaaaaaatg ggtggctcag caccaccaga tagcagctgg agaggaagtc 1150  
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 caaaaagtca agatgcacat ccactctacc aatgaagtga cgagaattta 1250  
 caatgtgata ggtactctca gaggagcagt ggaaccagac agatatgtca 1300  
 ttctgggagg tcaccgggac tcatgggtgt ttggtggtat tgaccctcag 1350  
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 aaaggaaggg tggagaccta gaagaacaat tttgtttgca agctgggatg 1450  
 cagaagaatt tggctcttctt ggttctactg agtgggcaga ggagaattca 1500  
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 agaaggaaac tacactctga gagttgattg tacaccgctg atgtacagct 1600  
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 ggcaaatctc tttatgaaag ttggactaaa aaaagtcctt cccagagtt 1700  
 cagtggcatg cccaggataa gcaaattggg atctggaaat gattttgagg 1750

tggttttcca acgacttgga attgcttcag gcagagcacg gtataactaaa 1800  
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tgaaacatat gagttggtgg aaaagtttta tgatccaatg tttaaatata 1900  
acctcactgt ggcccagggt cgaggagga tggtgtttga gctagccaat 1950  
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acagaaattg cttccaagtt cagtgcagaga ctccaggact ttgacaaaag 2150  
caaccaata gtattaagaa tgatgaatga tcaactcatg tttctggaaa 2200  
gagcatttat tgatccatta gggttaccag acaggccttt ttataggcat 2250  
gtcatctatg ctccaagcag ccacaacaag tatgcagggg agtcattccc 2300  
aggaatttat gatgctctgt ttgatattga aagcaaagtg gacccttcca 2350  
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caggcagctg cagagacttt gagtgaagta gcctaagagg attttttaga 2450  
gaatccgtat tgaatttgtg tggatatgtca ctcagaaaga atcgtaatgg 2500  
gtatattgat aaattttaaa attggtatat ttgaaataaa gttgaatatt 2550  
atatataa 2558

<210> 618

<211> 750

<212> PRT

<213> Homo Sapien

<400> 618

Met	Trp	Asn	Leu	Leu	His	Glu	Thr	Asp	Ser	Ala	Val	Ala	Thr	Ala
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Arg	Arg	Pro	Arg	Trp	Leu	Cys	Ala	Gly	Ala	Leu	Val	Leu	Ala	Gly
				20					25					30
Gly	Phe	Phe	Leu	Leu	Gly	Phe	Leu	Phe	Gly	Trp	Phe	Ile	Lys	Ser
				35					40					45
Ser	Asn	Glu	Ala	Thr	Asn	Ile	Thr	Pro	Lys	His	Asn	Met	Lys	Ala
				50					55					60
Phe	Leu	Asp	Glu	Leu	Lys	Ala	Glu	Asn	Ile	Lys	Lys	Phe	Leu	His
				65					70					75
Asn	Phe	Thr	Gln	Ile	Pro	His	Leu	Ala	Gly	Thr	Glu	Gln	Asn	Phe
				80					85					90

Gln	Leu	Ala	Lys	Gln	Ile	Gln	Ser	Gln	Trp	Lys	Glu	Phe	Gly	Leu		95	100	105
Asp	Ser	Val	Glu	Leu	Ala	His	Tyr	Asp	Val	Leu	Leu	Ser	Tyr	Pro		110	115	120
Asn	Lys	Thr	His	Pro	Asn	Tyr	Ile	Ser	Ile	Ile	Asn	Glu	Asp	Gly		125	130	135
Asn	Glu	Ile	Phe	Asn	Thr	Ser	Leu	Phe	Glu	Pro	Pro	Pro	Pro	Gly		140	145	150
Tyr	Glu	Asn	Val	Ser	Asp	Ile	Val	Pro	Pro	Phe	Ser	Ala	Phe	Ser		155	160	165
Pro	Gln	Gly	Met	Pro	Glu	Gly	Asp	Leu	Val	Tyr	Val	Asn	Tyr	Ala		170	175	180
Arg	Thr	Glu	Asp	Phe	Phe	Lys	Leu	Glu	Arg	Asp	Met	Lys	Ile	Asn		185	190	195
Cys	Ser	Gly	Lys	Ile	Val	Ile	Ala	Arg	Tyr	Gly	Lys	Val	Phe	Arg		200	205	210
Gly	Asn	Lys	Val	Lys	Asn	Ala	Gln	Leu	Ala	Gly	Ala	Lys	Gly	Val		215	220	225
Ile	Leu	Tyr	Ser	Asp	Pro	Ala	Asp	Tyr	Phe	Ala	Pro	Gly	Val	Lys		230	235	240
Ser	Tyr	Pro	Asp	Gly	Trp	Asn	Leu	Pro	Gly	Gly	Gly	Val	Gln	Arg		245	250	255
Gly	Asn	Ile	Leu	Asn	Leu	Asn	Gly	Ala	Gly	Asp	Pro	Leu	Thr	Pro		260	265	270
Gly	Tyr	Pro	Ala	Asn	Glu	Tyr	Ala	Tyr	Arg	Arg	Gly	Ile	Ala	Glu		275	280	285
Ala	Val	Gly	Leu	Pro	Ser	Ile	Pro	Val	His	Pro	Ile	Gly	Tyr	Tyr		290	295	300
Asp	Ala	Gln	Lys	Leu	Leu	Glu	Lys	Met	Gly	Gly	Ser	Ala	Pro	Pro		305	310	315
Asp	Ser	Ser	Trp	Arg	Gly	Ser	Leu	Lys	Val	Pro	Tyr	Asn	Val	Gly		320	325	330
Pro	Gly	Phe	Thr	Gly	Asn	Phe	Ser	Thr	Gln	Lys	Val	Lys	Met	His		335	340	345
Ile	His	Ser	Thr	Asn	Glu	Val	Thr	Arg	Ile	Tyr	Asn	Val	Ile	Gly		350	355	360
Thr	Leu	Arg	Gly	Ala	Val	Glu	Pro	Asp	Arg	Tyr	Val	Ile	Leu	Gly		365	370	375
Gly	His	Arg	Asp	Ser	Trp	Val	Phe	Gly	Gly	Ile	Asp	Pro	Gln	Ser				

	380		385		390
Gly Ala Ala Val	Val His Glu Ile Val	Arg Ser Phe Gly Thr	Leu		
	395	400	405		
Lys Lys Glu Gly	Trp Arg Pro Arg Arg	Thr Ile Leu Phe Ala	Ser		
	410	415	420		
Trp Asp Ala Glu	Glu Phe Gly Leu Leu	Gly Ser Thr Glu Trp	Ala		
	425	430	435		
Glu Glu Asn Ser	Arg Leu Leu Gln Glu	Arg Gly Val Ala Tyr	Ile		
	440	445	450		
Asn Ala Asp Ser	Ser Ile Glu Gly Asn	Tyr Thr Leu Arg Val	Asp		
	455	460	465		
Cys Thr Pro Leu	Met Tyr Ser Leu Val	His Asn Leu Thr Lys	Glu		
	470	475	480		
Leu Lys Ser Pro	Asp Glu Gly Phe Glu	Gly Lys Ser Leu Tyr	Glu		
	485	490	495		
Ser Trp Thr Lys	Lys Ser Pro Ser Pro	Glu Phe Ser Gly Met	Pro		
	500	505	510		
Arg Ile Ser Lys	Leu Gly Ser Gly Asn	Asp Phe Glu Val Phe	Phe		
	515	520	525		
Gln Arg Leu Gly	Ile Ala Ser Gly Arg	Ala Arg Tyr Thr Lys	Asn		
	530	535	540		
Trp Glu Thr Asn	Lys Phe Ser Gly Tyr	Pro Leu Tyr His Ser	Val		
	545	550	555		
Tyr Glu Thr Tyr	Glu Leu Val Glu Lys	Phe Tyr Asp Pro Met	Phe		
	560	565	570		
Lys Tyr His Leu	Thr Val Ala Gln Val	Arg Gly Gly Met Val	Phe		
	575	580	585		
Glu Leu Ala Asn	Ser Ile Val Leu Pro	Phe Asp Cys Arg Asp	Tyr		
	590	595	600		
Ala Val Val Leu	Arg Lys Tyr Ala Asp	Lys Ile Tyr Ser Ile	Ser		
	605	610	615		
Met Lys His Pro	Gln Glu Met Lys Thr	Tyr Ser Val Ser Phe	Asp		
	620	625	630		
Ser Leu Phe Ser	Ala Val Lys Asn Phe	Thr Glu Ile Ala Ser	Lys		
	635	640	645		
Phe Ser Glu Arg	Leu Gln Asp Phe Asp	Lys Ser Asn Pro Ile	Val		
	650	655	660		
Leu Arg Met Met	Asn Asp Gln Leu Met	Phe Leu Glu Arg Ala	Phe		
	665	670	675		





<210> 623  
<211> 25  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 623  
tgggaaatca ggaatggtgt tctcc 25

<210> 624  
<211> 50  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide probe

<400> 624  
cttgttttca ccattgggct aactttgctg ctaggagttc aagccatgcc 50